



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 147987

To: Sarvamangala Devi
Location: REM 3C18
Art Unit: 1645
Wednesday, March 16, 2005

Case Serial Number: 10/041775

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.



This Page Blank (uspto)

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	950	93.5	689	2	Q53599	staphylococ
2	950	93.5	689	2	Q924P5	staphylococ
3	950	93.5	689	2	Q6GPB8	staphylococ
4	907	89.3	584	2	Q9XAS5	staphylococ
5	888.5	87.5	687	2	Q9S224	staphylococ
6	886.5	87.3	657	2	Q07318	staphylococ
7	884.5	87.1	476	2	Q9GQ81	staphylococ
8	881.5	86.8	581	2	Q8NVR4	staphylococ
9	814.5	80.2	584	2	Q9K4S8	staphylococ
10	801.5	78.9	535	2	Q924J2	staphylococ
11	318	31.3	121	1	OMP7 STAAU	staphylococ
12	210	20.7	144	2	Q8NXX3	staphylococ
13	210	20.7	144	2	Q99VA9	staphylococ
14	210	20.7	144	2	Q7A6G0	staphylococ
15	210	20.7	144	2	Q6GUA5	staphylococ
16	210	20.7	144	2	Q6GTA6	staphylococ
17	146.5	14.4	141	2	Q8G961	staphylococ
18	146.5	14.4	141	2	Q99S64	staphylococ
19	146.5	14.4	141	2	Q7A090	staphylococ
20	146.5	14.4	141	2	Q7A483	staphylococ
21	146.5	14.4	141	2	Q6G7B0	staphylococ
22	144.5	14.2	141	2	Q6GBM4	staphylococ
23	136	13.4	106	2	Q99QS2	staphylococ
24	135	13.3	96	2	Q8NVR5	staphylococ
25	118	11.6	1178	2	Q7P8M0	fusobacteri
26	118	11.6	1620	2	Q81IV3	plasmodium
27	116	11.4	1792	2	Q81D94	plasmodium
28	115	11.3	374	2	Q8DVE1	streptococc
29	114.5	11.3	640	1	GYRB SPICI	streptococc
30	114.5	11.3	1272	2	Q9PR01	ureaplasma
31	113	11.1	1016	2	Q7PDP5	plasmodium

QY	4	SHHHHHGSGQIPYTIITVNGTSQNILSLTFKNKQOISYKDLENKVKSVLYFNRGISDIDL	63
Db	41	SLHHGYSKIQIPYTIITVNGTSQNILSLTFKNKQOISYKDLENKVKSVLYFNRGISDIDL	100
QY	64	RLSKQAKYTVHFKNKGTGRVVLDKAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ	123
Db	101	RLSKQAKYTVHFKNKGTGRVVLDKAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ	160
QY	124	VPYTIITVNGTSQNILSLTFKNKQOISYKDLENKVKSVLYFNRGISDIDL	183
Db	161	VPYTIITVNGTSQNILSLTFKNKQOISYKDLENKVKSVLYFNRGISDIDL	220
QY	184	NFKNGTKKVIDLKAGIY 200	
Db	221	NFKNGTKKVIDLKAGIY 237	
RESULT 4			
Q9XAS5		PRELIMINARY; PRT; 584 AA.	
AC	Q9XAS5		
DT	01-NOV-1999 (T-EMBLrel. 12, Created)		
DT	01-NOV-1999 (T-EMBLrel. 12, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Map-7 protein precursor.		
GN	Name=map-7;		
OS	Staphylococcus aureus.		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OC	NCBI_TaxID=1280;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	Russain Shaikh M., Heilmann C., Peters G., Herzman M.;		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR	ENBL; AJ243790; CAB50920.1; -.		
DR	Interpro; IPR005298; MAP.		
DR	Pfam; PF03642; MAP; 5.		
KW	Signal.		
FT	SIGNAL	1 30 Potential.	
FT	CHAIN	31 584 Potential.	
FT	SEQUENCE	584 AA; 65173 MW; 0A39383C55P639C1 CRC64;	
Query Match 89.3%; Score 907; DB 2; Length 584;			
Best Local Similarity 93.4%; Pred. No. 6.5e-53; Indels 0; Gaps 0;			
Matches 184; Conservative 3; Mismatches 10;			
QY	4	SHHHHHGSGQIPYTIITVNGTSQNILSLTFKNKQOISYKDLENKVKSVLYFNRGISDIDL	63
Db	41	SLHHGYSKIQIPYTIITVNGTSQNILSLTFKNKQOISYKDLENKVKSVLYFNRGISDIDL	100
QY	64	RLSKQAKYTVHFKNKGTGRVVLDKAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ	123
Db	101	RLSKQAKYTVHFKNKGTGRVVLDKAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ	160
QY	124	VPYTIITVNGTSQNILSLTFKNKQOISYKDLENKVKSVLYFNRGISDIDL	183
Db	161	VPYTIITVNGTSQNILSLTFKNKQOISYKDLENKVKSVLYFNRGISDIDL	220
QY	184	NFKNGTKKVIDLKAGIY 200	
Db	221	NFKNGTKKVIDLKAGIY 237	
RESULT 5			
Q9S224		PRELIMINARY; PRT; 687 AA.	
AC	Q9S224		
DT	01-MAY-2000 (T-EMBLrel. 13, Created)		
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)		
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)		
DE	Cell surface protein map-w precursor.		
GN	Name=map-w;		
OS	Staphylococcus aureus.		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		

```

OX NCBI_TaxID=1280;
RN [1]_TaxID=1280;
RP SEQUENCE FROM N.A.
RC STRAIN=wood 46;
RA Hussein Shaikh M., Heilmann C., Peters G., Herrmann M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ245439; CAB51807.1; -.
DR InterPro; IPR005298; MAP.
DR Pfam; PF03642; MAP; 6.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 687 AA; 77072 MW; 91D429532DB7DD2B CRC64;

Query Match 87.5%; Score 886.5; DB 2; Length 687;
Best Local Similarity 91.3%; Pred. No. 1.4e-51;
Matches 178; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 6 HHHHGSQIPYITVNGTSQNTLSSTFNKNQOISYKDIEKNVSVLYFNRGISDIDLRL 65
DB 43 HHGHSNIQIPYITVNGTSQNTLSSTFNKNQOISYKDIEKNVSVLYFNRGISDIDLRL 102
QY 66 SKQAKYTVHFKNKGRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVP 125
DB 103 SKQAEYTVHFKNKGRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVP 161
QY 126 YTITVNGTSQNTLSNLTFFKNQOISYKOLENNVSVLKSNRGITDVLRLSKQAKFTVNF 185
DB 162 YTITVNGTSQNTLSNLTFFKNQOISYKOLENNVSVLKSNRGITDVLRLSKQAKFTVNF 221
QY 186 KNGTKKVIDLKAGIY 200
DB 222 KNGTKKVIDLKAGIY 236

RESULT 6
O07318
ID O07318 PRELIMINARY; PRT; 657 AA.
AC O07318;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Outer surface binding 70kD protein (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]_TaxID=1280;
RP SEQUENCE FROM N.A.
RC STRAIN=wood 46;
RA Yousef Y., Draeger R., Schiltz M., Peter H., Schlesier M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y10419; CAAY71446.1; -.
DR InterPro; IPR005298; MAP.
DR Pfam; PF03642; MAP; 6.
FT NON_TER 1
SQ SEQUENCE 657 AA; 74044 MW; 1A7980DF1B7E09A3 CRC64;

Query Match 87.3%; Score 886.5; DB 2; Length 657;
Best Local Similarity 90.8%; Pred. No. 1.8e-51;
Matches 177; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

QY 6 HHHHGSQIPYITVNGTSQNTLSSTFNKNQOISYKDIEKNVSVLYFNRGISDIDLRL 65
DB 13 HHGHSNIQIPYITVNGTSQNTLSSTFNKNQOISYKDIEKNVSVLYFNRGISDIDLRL 72
QY 66 SKQAKYTVHFKNKGRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVP 125
DB 73 SKQAEYTVHFKNKGRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVP 131
QY 126 YTITVNGTSQNTLSNLTFFKNQOISYKOLENNVSVLKSNRGITDVLRLSKQAKFTVNF 185
DB 132 YTITVNGTSQNTLSNLTFFKNQOISYKOLENNVSVLKSNRGITDVLRLSKQAKFTVNF 191
QY 186 KNGTKKVIDLKAGIY 200
DB 222 KNGTKKVIDLKAGIY 236
```

```

DB 192 KNGTKKVIDLKAGIY 206

RESULT 7
Q99QS1
ID Q99QS1 PRELIMINARY; PRT; 476 AA.
AC Q99QS1;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Truncated map-w protein.
GN OrderedLocNames=SAV1938;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=159878;
RN [1]_TaxID=159878;
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003364; BAB58100.1; -.
DR InterPro; IPR005298; MAP.
DR Pfam; PF03642; MAP; 4.
KW Complete proteome.
SQ SEQUENCE 476 AA; 53377 MW; 04E6B5C9DBD782E8 CRC64;

Query Match 87.1%; Score 884.5; DB 2; Length 476;
Best Local Similarity 90.8%; Pred. No. 1.7e-51;
Matches 177; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 6 HHHHGSQIPYITVNGTSQNTLSSTFNKNQOISYKDIEKNVSVLYFNRGISDIDLRL 65
DB 43 HHGHSNIQIPYITVNGTSQNTLSSTFNKNQOISYKDIEKNVSVLYFNRGISDIDLRL 102
QY 66 SKQAKYTVHFKNKGRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVP 125
DB 103 SKQAEYTVHFKNKGRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKAKANVQVP 161
QY 126 YTITVNGTSQNTLSNLTFFKNQOISYKOLENNVSVLKSNRGITDVLRLSKQAKFTVNF 185
DB 162 YTITVNGTSQNTLSNLTFFKNQOISYKOLENNVSVLKSNRGITDVLRLSKQAKFTVNF 221
QY 186 KNGTKKVIDLKAGIY 200
DB 222 KNGTKKVIDLKAGIY 236

RESULT 8
Q8NVR4
ID Q8NVR4 PRELIMINARY; PRT; 581 AA.
AC Q8NVR4;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Truncated cell surface protein map-w.
GN Name=truncated map-w; OrderedLocNames=MW1880;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]_TaxID=196620;
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
```

RA	Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,	
RA	Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,	
RA	Yamamoto K., Hiramatsu K.,	
RT	"Genome and virulence determinants of high virulence community-	
RT	acquired MRSA."	
RL	Lancet 359:1819-1827(2002).	
DR	EMBL; AP004828; BAB95745.1; -.	
DR	InterPro; IPR005298; MAP.	
DR	Pfam; PF03642; MAP; 5.	
KW	Complete proteome.	
SQ	SEQUENCE 581 AA; 65095 MW; 912F70CDAD8B8C68 CRC64;	
Query Match 86.8%; Score 881.5; DB 2; Length 581;		
Best Local Similarity 90.3%; Pred. No. 3.3e-51;		
Matches 176; Conservative 8; Mismatches 10; Indels 1; Gaps 1;		
Qy	6 HHHHGSQIPYITVNGTSQNLSTFNKNQOISYKDIENKVSVLVFNRGISDIDLRL	65
Db	43 HGHNSNIQIPYITVNGTSQNLSTFNKNQOISYKDIENKVSVLVFNRGISDIDLRL	102
Qy	66 SKQAKYTVHFKNKGRVVDLKGAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKANQVP	125
Db	103 SKQAEYTVHFKNKGVKVIDLKSIGIYTDLINTSDIKAISVNVDTKKQPKDK-AKANQVP	161
Qy	126 YTIITVNGTSQNLSTFNKNQOISYKDLNKNVSVLKSNGRITDVLRLSKQAKFTVNF	185
Db	162 YTIITVNGTSQNLSTFNKNQOISYKDLGKVSLSNRGITDVLRLSKQAKYTVNF	221
Qy	186 KNGTKKVIDLKAGIY 200	
Db	222 KNGTKKVIDLKSGIY 236	
RESULT 9		
ID	Q9K4S8 PRELIMINARY; PRT; 584 AA.	
AC	Q9K4S8;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Map-ND2C protein precursor.	
GN	Name=map-ND2C;	
OS	Staphylococcus aureus.	
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.	
OX	NCBI_TaxID=1280;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Newman;	
RC	MEDLINE=21546656; PubMed=11687475;	
RX	Hussain M., Becker K., von Eiff C., Peters G., Herrmann M.;	
RA	"Analogues of Sap protein are conserved and prevalent in clinical	
RT	Staphylococcus aureus isolates."	
RL	Clin. Diagn. Immunol. 8:1271-1276(2001).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Newman D2C ATCC 25904;	
RC	Hussain Shaikh M.;	
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AJ290973; CAB94853.1; -.	
DR	InterPro; IPR005298; MAP.	
DR	Pfam; PF03642; MAP; 5.	
KW	Signal.	
FT	SIGNAL 1 30 Potential.	
FT	CHAIN 31 584 Map-ND2C protein.	
SQ	SEQUENCE 584 AA; 65542 MW; EFE45AC0C9615ED6 CRC64;	
Query Match 80.2%; Score 814.5; DB 2; Length 584;		
Best Local Similarity 81.8%; Pred. No. 1e-46;		
Matches 162; Conservative 19; Mismatches 16; Indels 1; Gaps 1;		
Qy	4 SHHHHGHSGQIPYITVNGTSQNLSTFNKNQOISYKDIENKVSVLVFNRGISDIDL	63
Db	41 SLHHGYSKVHVPYAITVNGTSQNLSTFNKNQOISYKDLGKVSLSNRGITDVLRLSKQAKYTVNF	100
Qy	64 RLSKQAKYTVHFKNKGRVVDLKGAGIHTADLINTSDIKAISVNVDTKKQVKDKEA-KANV	122
Db	101 RLSKQAKYTVHFKNKGRVVDLKGAGIHTADLINTSDIKAISVNVDTKKQVKDKEA-KANV	160
Qy	123 QVPYITVNGTSQNLSTFNKNQOISYKDLNKNVSVLKSNGRITDVLRLSKQAKFT	182
Db	161 QVPYITVNGTSQNLSTFNKNQOISYKDLGKVSLSNRGITDVLRLSKQAKYTVNF	220
Qy	183 VNFKNKTKKVIDLKAGIY 200	
Db	221 VNFKNKTKKVIDLKSGIY 238	
RESULT 10		
ID	Q9Z4J2 PRELIMINARY; PRT; 535 AA.	
AC	Q9Z4J2;	
DT	01-MAY-1999 (TrEMBLrel. 10, Created)	
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Map protein (Fragment).	
GN	Name=map;	
OS	Staphylococcus aureus.	
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.	
OX	NCBI_TaxID=1280;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Newman;	
RC	Kreikemeyer B., McDevitt D., Kapur V., Hook M.;	
RL	Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AJ223806; CAA11555.1; -.	
DR	InterPro; IPR005298; MAP.	
DR	Pfam; PF03642; MAP; 5.	
FT	NON_TER 1 535 Map protein.	
FT	CHAIN <1 535	
SQ	SEQUENCE 535 AA; 60459 MW; D2566318AC64F2A1 CRC64;	
Query Match 78.9%; Score 801.5; DB 2; Length 535;		
Best Local Similarity 84.6%; Pred. No. 7.1e-46;		
Matches 159; Conservative 19; Mismatches 9; Indels 1; Gaps 1;		
Qy	14 IPYITVNGTSQNLSTFNKNQOISYKDIENKVSVLVFNRGISDIDLRLSKQAKYTV	73
Db	2 VPYAITVNGTSQNLSTFNKNQOISYKDLGKVSLSNRGITDVLRLSKQAKYTV	61
Qy	74 HFKNGTKRVDLKGAGIHTADLINTSDIKAISVNVDTKKQVKDKEA-KANVQVPYITVNG	132
Db	62 YFKNGTKRVDLKGAGIHTADLINTSDIKAISVNVDTKKQVKDKEA-KANVQVPYITVNG	121
Qy	133 TSQNLSTFNKNQOISYKDLNKNVSVLKSNGRITDVLRLSKQAKFTVNFKNGT	192
Db	122 TSQNLSTFNKNQOISYKDLGKVSLSNRGITDVLRLSKQAKYTVNFKNGT	181
Qy	193 IDLKAGIY 200	
Db	182 IDLKSGIY 189	
RESULT 11		
ID	OMP7_STAAU STANDARD; PRT; 121 AA.	
AC	P21223;	
DT	01-MAY-1991 (Rel. 18, Created)	
DT	01-MAY-1991 (Rel. 18, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	70 Kda outer membrane protein precursor (Fragment).	
OS	Staphylococcus aureus.	
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.	
OX	NCBI_TaxID=1280;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=COL;	

```

RX MEDLINE=89263748; PubMed=2726469;
RA Projan S.J., Kornblum J., Kreiswirth B., Moghazeh S.L., Eisner W.,
RA Novick R.P.;
RT "Nucleotide sequence: the beta-hemolysin gene of Staphylococcus
RT aureus.";
RN Nucleic Acids Res. 17:3305-3305(1989).
RN [2]
RP SEQUENCE OF 31-52.
RP STRAIN=ATCC 25923;
RA Yousef Y., Schiltz E., Vogt A.;
RL Submitted (MAR-1991) to Swiss-Prot.
RN [3]
RP SEQUENCE OF 31-53.
RP STRAIN=Newman;
RA Hussein M.S., Herrmann M., Chhatwal G.S., Peters G.;
RT "Map-n protein deficient mutant of Staphylococcus aureus Newman binds
RT less to fibronection and collagen coated surfaces. A 70 kDa vitronectin
RT protein of Staphylococcus aureus Newman.";
RL Submitted (FEB-1999) to Swiss-Prot.
CC -!- FUNCTION: Binds various plasma and ECM-proteins.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X13404; CAA31768.1; -.
DR PIR; S15765; S15765.
DR InterPro; IPR005298; MAP.
DR Pfam; PF03642; MAP; 1.
KW Direct protein sequencing; Outer membrane; Signal.
FT SIGNAL 1 30
FT CHAIN 31 >121 70 kDa outer membrane protein.
FT VARIANT 111 111 Y -> S (in strain UM4102).
FT VARIANT 111 111 Y -> F (in strain UM4082).
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13240 MW; DCFE33E806241E4A CRC64;
-----
Query Match 31.3%; Score 318; DB 1; Length 121;
Best Local Similarity 76.5%; Pred. No. 3.7e-14;
Matches 62; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
QY 4 SHHHHHSQIPYITVNGTSQNLSSLTFFNKNQOISYKDIENKVKSVLYFNRGISDIDL 63
Db 41 SLHHGYSKVHPYAITVNGTSQNLSSLTFFNKNQOISYKDLDRVKSVLKSDRGISDIDL 100
QY 64 RLSKQAKTVVHPKNGTKRVVD 84
Db 101 RLSKQAKTVVFPKNGTKKVID 121
-----
Query Match 31.3%; Score 318; DB 1; Length 121;
Best Local Similarity 76.5%; Pred. No. 3.7e-14;
Matches 62; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
QY 4 SHHHHHSQIPYITVNGTSQNLSSLTFFNKNQOISYKDIENKVKSVLYFNRGISDIDL 63
Db 41 SLHHGYSKVHPYAITVNGTSQNLSSLTFFNKNQOISYKDLDRVKSVLKSDRGISDIDL 100
QY 64 RLSKQAKTVVHPKNGTKRVVD 84
Db 101 RLSKQAKTVVFPKNGTKKVID 121
-----
RESULT 12
Q8NKE3 PRELIMINARY; PRT; 144 AA.
AC Q8NKE3;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MW0863 protein.
GN OrderedLocusNames=MW0863;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,

```

```

RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004825; BAB94728.1; -.
DR InterPro; IPR005298; MAP.
DR Pfam; PF03642; MAP; 1.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15838 MW; F29A2AE30ECD4563 CRC64;
-----
Query Match 20.7%; Score 210; DB 2; Length 144;
Best Local Similarity 44.3%; Pred. No. 8.1e-07;
Matches 43; Conservative 22; Mismatches 32; Indels 0; Gaps 0;
QY 14 IPYITVNGTSQNLSSLTFFNKNQOISYKDIENKVKSVLYFNRGISDIDLRLSKQAKTV 73
Db 48 VPYITVNGTSQNLSSLTFFNKNQOISYKDLGNKVKALLYDERGVTPEKIRNAKSAVYTI 107
QY 74 HFKNGTGRVVDLKAGIHTADLINTSDIKAISVNVDTK 110
Db 108 TWKDGSKKEVDLKKDSYTNLFDNSIKQIDINVTK 144
-----
RESULT 13
Q99VA9 PRELIMINARY; PRT; 144 AA.
AC Q99VA9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SAV0981;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Goto S.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogatawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003360; BAB57143.1; -.
DR PIR; F89865; F89865.
DR InterPro; IPR005298; MAP.
DR Pfam; PF03642; MAP; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 144 AA; 15898 MW; ABFE3FE30ED9506C CRC64;
-----
Query Match 20.7%; Score 210; DB 2; Length 144;
Best Local Similarity 44.3%; Pred. No. 8.1e-07;
Matches 43; Conservative 22; Mismatches 32; Indels 0; Gaps 0;
QY 14 IPYITVNGTSQNLSSLTFFNKNQOISYKDIENKVKSVLYFNRGISDIDLRLSKQAKTV 73
Db 48 VPYITVNGTSQNLSSLTFFNKNQOISYKDLGNKVKALLYDERGVTPEKIRNAKSAVYTI 107
QY 74 HFKNGTGRVVDLKAGIHTADLINTSDIKAISVNVDTK 110
Db 108 TWKDGSKKEVDLKKDSYTNLFDNSIKQIDINVTK 144
-----
RESULT 14
Q7A6G0 PRELIMINARY; PRT; 144 AA.
ID Q7A6G0
AC Q7A6G0;

```



```

RESULT 24
QBNVRS
ID QBNVRS PRELIMINARY; PRT; 96 AA.
AC QBNVRS;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Truncated map-w protein.
GS Name=truncated map-W; OrderedlocusNames=MW1879;
OS Staphylococcus aureus (strain MW2)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=156620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004828; BAB95744.1; -.
DR InterPro; IPR005298; MAP.
DR Pfam; PF03642; MAP; 1.
KW Complete proteome.
SQ SEQUENCE 96 AA; 11160 MW; DA9121B77B64FA51 CRC64;

Query Match 13.3%; Score 135; DB 2; Length 96;
Best Local Similarity 28.3%; Pred. No. 0.055;
Matches 26; Conservative 25; Mismatches 41; Indels 0; Gaps 0;

Qy 16 YTTVNGTSQNLSTFNKNQOISYKDIENKVKSVLYFNRGISDIDLRLSKQAKYTVHF 75
Db 3 PVPVINKENIVSEFVYNASKITINDLSLKLSAIAANDQITIKHDIELAEAVKVIYF 62

Qy 76 KNGTKRVVDLKAGIHTADLINTSDIKATSVNV 107
Db 63 KNGSKSYVDLKTVEKDERVFRATDIKKVDIEL 94

RESULT 25
Q7P8M0 PRELIMINARY; PRT; 1178 AA.
AC Q7P8M0;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein.
GS Name=FN2276;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49256;
RA Kapatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haseelkorn R., Overbeek R., Kyrpides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABF01000001; EAA25241.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1178 AA; 134211 MW; 8C143D8C030F952D CRC64;

Query Match 11.6%; Score 118; DB 2; Length 1178;
Best Local Similarity 22.2%; Pred. No. 13;
Matches 47; Conservative 35; Mismatches 70; Indels 60; Gaps 7;

Qy 18 ITVNGTSQNLSTFNKNQOISYKDIENK-VKSVLYF--NRGISDIDLRLSKQAKYTVH 74
Db 2 ISFDRVDENILNKIIPREKKDLKNIKIDIKTIVHYSNDRGLS----- 46

Qy 75 FNGTKRVVDLKAGIHTADLINTSDIKATSVNVVDTKQVKQKAEKANVQVPTIYVNGTS 134
Db 47 -----IKTTMKPNDSEFGIELN-DFNLVSSKGGKNNLSARILTKVKGIP 91

Qy 135 QNLSNLTFKKQ-----QISYKDLNNVKSVLKSN--RGITDVLRL 175
Db 92 ENIALSVENKQNTDIIILAKSPKQNTIPDINIRGKIENQKDLKANIDSIVDFNWDY 151

Qy 176 SKQA-----KFTVNFKNGTKKVIDLKAGI 199
Db 152 KKDKKLAKIYGNKFTINVDVKKLTDCGRI 183

RESULT 26
Q8IIV3 PRELIMINARY; PRT; 1620 AA.
AC Q8IIV3;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein.
GS ORFNames=PF11_0060;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan W.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perteira M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AE014836; AAN35649.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR ProDom; PD000001; Prot_kinase; 2.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1620 AA; 195179 MW; CB758269933C016 CRC64;

Query Match 11.6%; Score 118; DB 2; Length 1620;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 46; Conservative 40; Mismatches 81; Indels 26; Gaps 9;

Qy 9 HGSQIPYTTIVNGTSQNLSTFNKNQOISYKDIENKVKSVLYFNRGISDIDLRLSK 67
Db 1158 YHPSNGNIFITTKHLSNTYSN---ERFIELFNVQKKKKILSFHNSFEPIINNN 1214

Qy 68 QAKYTVHFNGTKRVVDLKAGIHTADLINTSDIKATSVNVVDTKQVKD-----KE 117
Db 1215 KIQINQVIQGNLHLQNIKKDIHS---INKELDIKKNNENQNNQNNQNNQYVYHQ 1271

```

Qy	118	AKANVQPYTYITVNGTSONILSNLTFKKNQOISYKDIENNVSUJLKSNGRGTITDVLBSK	177
Db	1272	NOTNLXP-NIMVKGKQN--ENESEYKKNNEIKYKNEENNINTIQHNNHNI-----QIYK	1324
Qy	178	QAKFTVNFKNGTK	190
Db	1325	DKR--INFMPHK	1335
RESULT 27			
Q81D94	PRELIMINARY; PRT; 1792 AA.		
ID	Q81D94		
AC	Q81D94		
DT	01-MAR-2003	(TrEMBLrel. 23, Created)	
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)	
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)	
DE	Malaria antigen.		
GN	Name=MAL13PI.304;		
OS	Plasmodium falciparum (isolate 3D7).		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
OX	NCBI_TaxId=36329;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,		
RA	Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,		
RA	Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;		
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL844509; CAD52732.1; -.		
DR	InterPro; IPRO11591; Botulinum.		
DR	ProDom; PD001963; Botulinum; 1.		
SO	SEQUENCE 1792 AA; 210163 MW; 4959BS2BS95SD9794 CRC64;		

[illegible]

```

RESULT 28
Q8DVE1
ID Q8DVE1 PRELIMINARY; PRT; 374 AA.
AC Q8DVE1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative cell division protein FtsQ (DivIB).
GN Name=ftsQ; OrderedLocusNames=SMU.550;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype c;
RX MEDLINE=22295063; PubMed=1239718; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,

```

```

RA Ferretti J.J.;
RT "genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR EMBL; AE014899; AAN58292.1; -.
DR InterPro; IPR005548; FtsQ.
DR Pfam; PF03799; FtsQ; 1.
KW Complete proteome.
SQ SEQUENCE 374 AA; 42515 MW; 9F69E3759232FC08 CRC64;

Query Match 11.3%; Score 115; DB 2; Length 374;
Best Local Similarity 24.2%; Pred. No. 5.8;
Matches 59; Conservative 42; Mismatches 63; Indels 58; Gaps 13;

QY 18 ITVNGTSQNLSSLTFNKQOISYKDIEKNVKSVLV-----FNRGISDIDLRLSKQAKYTV 73
DB 131 ITVSGNKNATIESOLI-----EELGIKK-SDYITLTLLFOANFERNILSKD-KWVKEAKLVY 184

QY 74 HFKNG-TKRYVD-----LKAGIHTADLINTSDIKA--ISVNVDTKKQVK 114
DB 185 HFPNHFTRLRVEYRIITAYRTQDKGYVPILENGTR-VDTVNASLPGSFVTINLDQEKVR 243

QY 115 -----DKEAKANVOVPYITTVNGTSQNLISNLTFFKNQOISYKDLNNYKSVLKSN 165
DB 244 ELVQKLAKLQKSLVGSIKV--ISSVNSSSTPKDLLLEMDKN-----NSVRVPL--- 289

QY 166 RGTTDVDLRLSKQAKFTVNFKNGTCKKVIDLKAGIY 200
DB 290 ---SEIDTKLPYYSKIKNLTQGS--IVDMEVGIIY 319

RESULT 29
GYRB SPICI STANDARD; PRT; 640 AA.
AC P34031;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA gyrase subunit B (EC 5.99.1.3).
GN Name=GyrB;
OS Spiroplasma citri.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Spiroplasmataceae; Spiroplasma.
OX NCBI_TaxID=2133;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R8A2HP;
RX MEDLINE=94290261; PubMed=7764984;
RA Ye F., Renaudin J., Bove J.M., Laigret F.;
RT "Cloning and sequencing of the replication origin (oriC) of the
RT Spiroplasma citri chromosome and construction of autonomously
RT replicating artificial plasmids.";
RL Curr. Microbiol. 29:23-29 (1994).
CC -1- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Made up of two chains. The A chain is responsible for DNA
CC breakage and rejoining; the B chain catalyzes ATP hydrolysis. The
CC enzyme forms an A2B2 tetramer.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; Z19108; CAA79523.1; -.

```

DR PIR: S35734; S35734.
DR HSP: P06982; 1A26.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR002288; DNA_gyraseB_C.
DR InterPro: IPR000565; DNA_gyrB.
DR InterPro: IPR001241; DNA_topoisom.
DR InterPro: IPR006171; Toprim_dom.
DR Pfam: PF00204; DNA_gyraseB_1.
DR Pfam: PF00986; DNA_gyraseB_C_1.
DR Pfam: PF02518; HATPase_C_1.
DR Pfam: PF01751; Toprim_1.
DR PRINTS: PR00418; TP12FAMILY.
DR ProDom: PD149633; DNA_gyrase_B_1.
DR SMART: SM00387; HATPase_C_1.
DR SMART: SM00433; TOP2C_1.
DR TIGRFAMs: TIGR01059; gyrB_1.
DR PROSITE: PS00177; TOPOISOMERASE_II; 1.
KW ATP-binding; Isomerase; Topoisomerase.
SQ SEQUENCE 640 AA; 72763 MW; A7403DE2B098D25A CRC64;

Query Match 11.3%; Score 114.5; DB 1; Length 640;
Best Local Similarity 24.5%; Pred. No. 12;
Matches 52; Conservative 50; Mismatches 61; Indels 49; Gaps 14;

QY 9 HHGQIPYITVNGTSQNLSLTFTKQOI-----SYKDLENKVKSVLYFNRG--IS 59
Db 145 HNGGQLTPIKVGSTGTGTTVLPDEKIPKETTIFSTIQNRKQLVFLNKGLEIS 204
QY 60 DIDRLSKQAKYTVH-FKNGTK-RVVDLKAGIHTADLINTSDIKAKISVNVDTKKQVKKE 117
Db 205 LVDLREDEEKTVLQFNGIKDYVLELTKTIGTP-----LNDVFVY-----EGIED-- 251
QY 118 AKANVOQPYITVNGT-SQNILS-----TLFKNQOIS-YKDLNNVKS-VLKS 165
Db 252 ---NIWVEFGLOYNDYSENIFSPFCNINTHGEGTHEGALAIIVREINNYFKNQINKON 308
QY 166 RGITVDLRLSKQAKET-VFKNGTKYKVIDLK 196
Db 309 KGNED-----KFTWDDIKEGMTIISIR 331

RESULT 30
QSPR01 PRELIMINARY; PRT; 1272 AA.
ID Q9PR01
AC Q9PR01;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Conserved hypothetical.
GN OrderedLocusNames=U0143;
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 700970;
RX MEDLINE=20500219; PubMed=11048724; DOI=10.1038/35037619;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
urealyticum.";
RL Nature 407:757-762(2000).
DR EMBL; AE002115; AAF30549.1; -.
DR InterPro: IPR011591; Botulinum.
DR ProDom: PD001963; Botulinum; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1272 AA; 149378 MW; B110E502B96770F9 CRC64;

Query Match 11.3%; Score 114.5; DB 2; Length 1272;
Best Local Similarity 25.0%; Pred. No. 25;
Matches 52; Conservative 36; Mismatches 69; Indels 51; Gaps 11;

QY 14 IPYITVNGTSQNLSLTFTKQOISYKDLENKVKSVLYFNRGISDIDLRLSKQAKYTV 73

Db 637 IPYSL-----RNLI-SUTLHEREYAIYK--HNATNGFVLYNTITSNKDFNLKKNKESY 687
QY 74 HFKN-----GTRKRVLDLKG-----IHTADLINTSDIKAKISVNVDT----- 109
Db 688 HNLNLIHLAIATKDEGLKK--DESAGFFLEKLDLNDPDLNLFKDEIDIVFNVDELDPNLIY 745
QY 110 KKQVKQKE-AKANVOQPYITVNGTSQNLSLTFTKQOISYKDLENKVKSVLYFNRG 168
Db 746 ESQVLDKMRSHVPIPIYKVI-KKHILEDVEFSLNLYALGSEAYENHIYQOIKS----- 800
QY 169 TDVDLRLSKQAKETVFNKNGTKKVIDLK 196
Db 801 -----QLKFNV-FLNGSKIKVEVK 818

RESULT 31
Q7PDP5 PRELIMINARY; PRT; 1016 AA.
ID Q7PDP5
AC Q7PDP5;
DT 01-MAR-2004 (TremBLrel. 26, Created)
DT 01-MAR-2004 (TremBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Erythrocyte membrane protein PFEMP3.
GN Name=PY03960;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow J.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL0100183; EAL15755.1; -.
SQ SEQUENCE 1016 AA; 119602 MW; 1C33F4AE66E30413 CRC64;

Query Match 11.1%; Score 113; DB 2; Length 1016;
Best Local Similarity 22.0%; Pred. No. 25;
Matches 54; Conservative 39; Mismatches 83; Indels 70; Gaps 11;

QY 8 HHGQIPYITVNGTSQNLSLTFTN-----KNQOISYKDLENKVKSVLYFNRG--- 57
Db 422 HNLNKKI-NKITINGEYNELIKS--FNSKTRNTQNIKNQIRHLEDQVDNVLMMQKSDNL 478
QY 58 ---TSDIDLRLSKQA-----KYTVHFK-----NGTKRVVDLKAGIHTADLINT 97
Db 479 FIKINDYINNLNQIGSFILNNQFLHHNENNNYNDNNNGTKETINV--DVHNYKEIQN 536
QY 98 SDI-----KAISVNVDTKKQVK-----DKEAKANVOQPYITVNGTSQNIL 138
Db 537 TDISKKNSFIHKCNIDIKYDHKKKKVNNQIYDDNNGKRSLSIQKCIENYHNENN 596
QY 139 SNLTFK-----KNQOISYKDLENKVKSVLKSNGITDIDLRLSKQAKYTVNF 185
Db 597 NNSYKKTDTIQSAQSVYSDKNENDYKNLYNDEKFLYLNKLI---ELKTSKMKQLNI 653
QY 186 KNGTKK 191

RT	parasite Plasmodium yoelii yoelii.";
RL	Nature 419:512-519(2002).
CC	-!- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBS whole genome shotgun (WGS) entry which is
CC	preliminary data.
ENBL; AABL01000239; EAA19159.1; -.	
DR InterPro; IPR003900; KID_repeat.	
DR Pfam; PF02524; KID; 9.	
KW Hypothetical protein.	
SQ SEQUENCE 2341 AA; 266712 MW; 51D2041A084F4BA5 CRC64;	
Query Match	11.1%; Score 112.5; DB 2; Length 2341;
Best Local Similarity	27.0%; Pred. No. 69;
Matches	54; Conservative 37; Mismatches 80; Indels 29; Gaps 11;
Qy	21 NGTSONILSSLTFTNKQOISYKDIENK-----VKSVLVFNRGISDIDLRLSKQAQVTYH 74
Dd	502 NKESKNIESNTDVKNKESENTDVKNKESENINVKNAEKAKDKVKKDKV-KNEAE-NID 559
Qy	75 FKGTKRVVDLK-AGIHTADLINTSDIKAISVNVDTK-----OVKDKRKANVQVPYT 127
Dd	560 AENEDAENTDVKNDAENEDAEITDVKNKESENINVKNIDAENTHVKNKESK-NVDAENT 618
Qy	128 ITVNGTSONI-LNLTFK-----KNQOISYKYLEN-----NVKSVLSNRGITDIDLRLS 176
Dd	619 YVKNKAENTHVKNKESKNIDVKNKAENKODTVDVKNKDAENIDAENEDAEITDVK-N 677
Qy	177 QKQFTVFNFKNGTCKVIDLK 196
Dd	678 RDAENTY-VKNKESENIDVK 696
RESULT 34	
Q9YVT6	PRELIMINARY; PRT; 1127 AA.
ID	Q9YVT6
AC	Q9YVT6;
DT	01-MAY-1999 (TrEMBLrel. 10, Created)
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Hypothetical protein MSV156.
OS	Name=MSV156;
GN	Melanoplus sanguinipes entomopoxvirus (MsEPV).
OC	viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OX	Entomopoxvirus B.
NCBI_Taxid=83191;	
[1]	
RN	SEQUENCE FROM N.A.
FX	MEDLINE=99102612; PubMed=9847359;
RA	Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
RT	"The Genome of Melanoplus sanguinipes entomopoxvirus.";
J. Virol. 73:533-552(1999).	
RL	EMBL; AF063866; AAC97677.1; -.
DR	PIR; T28317; T28317.
KW	Hypothetical protein.
SQ	SEQUENCE 1127 AA; 134265 MW; F185DA1DSA3FE7D1 CRC64;
Query Match	11.0%; Score 112; DB 2; Length 1127;
Best Local Similarity	23.3%; Pred. No. 32;
Matches	47; Conservative 40; Mismatches 81; Indels 34; Gaps 9;
Qy	20 VNGTSQNILSSLTFN-QNQOTSYKDIENTKVSVLYFNRGISDIDLRLSKQAQYTVHPKNG 78
Dd	177 VSSEKQLIEQIYKNNKEIFPKNIENVQKEI---NKKQDELNKLDESKEFIKKQE 233
Qy	79 TKRVVDLKAGIHATDLINTSDIKAISVNVDTKQVKK-D-EKAN-----QVQPYTIT 129
Dd	234 LNKTIIDKK----QBELIKGLNDKEINFNIDEKQKLDLOINSKTNLNENIKGVNNILTYET 289
Qy	130 VNGTSQNILSLTFKNQQOISYKD-----LENNVKSVL-----KSNRGITDIDLRLSK 177
Dd	290 KNKLSN--LQNEILNKDSTIKSLDEKQKLLDELKNINNITSLVNKSNTKITNIQOLLES 347
Qy	178 QAKFTVNFKNGTCKVIDLKAGI 199


```

RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
RL EMBL; AE014833; AAN35462.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1811 AA; 216655 MW; 8A25116576D5FED1 CRC64;

Query Match 10.9%; Score 111; DB 2; Length 1811;
Best Local Similarity 23.4%; Pred. No. 65;
Matches 60; Conservative 34; Mismatches 74; Indels 88; Gaps 14;

QY 6 HHHHGSQIPYITVN-----GTSQNILSS-----LTFKKNQIISYKDI 44
Db 1404 HNHVDGNIILTWNNINISLTLGSKNNFVSPPEKTHTKIPEPILFNMNQ---KDV 1460
QY 45 ENK-----KSVLYFNRGISDIDLRLS---KQAKYTVH-----FKNG-----TK 80
Db 1461 QNKNQVDYIDILFSTGFCDFISVTCGIYRKKYTCYNISTIPWFGYKNWGLVNCMKK 1520
QY 81 RVVDLKAGIHTADLINTSDIKAISVNVDTKKVQKDKAKANVQVPYITVNGTSQNILSN 140
Db 1521 DMVSIIRIDH--DIKEKNEIKELYN--NIISQIKDK--KNTYK-----N 1559
QY 141 LTFKKNQIISYKDLNNV-----KSVLSKNRGITVDVLRLSKQAKFTVN 184
Db 1560 VNLSHDQNDYKD--SNNVFINQDNKLYQHNIAYNKEIQKN--IIYIDDNKKKKESNN 1616
QY 185 FKNGTKKKVIDLKAGIY 200
Db 1617 MSIKKNLYEKKNVY 1632

RESULT 38
Q81581 PRELIMINARY; PRT; 3896 AA.
AC Q81581
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN ORFNames=PFL1645;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]

SEQUENCE FROM N.A.
RP MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Hyman R.W., Fung E., Conway A., Kurdi O., Mao J., Miranda M.,

```

```

RA Nakao B., Rowley D., Tamaki T., Wang F., Davis R.W.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014849; AAN36415.1; -.
DR HSSP; Q92831; 1N72.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR000875; Cecropin.
DR Pfam; PF00439; Bromodomain; 1.
DR PRINTS; PR00503; Bromodomain; 1.
DR SMART; SM00297; BRMO; 1.
DR PROSITE; PS00014; BROMODOMAIN 2; 1.
DR PROSITE; PS00268; CECROPIN; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 3896 AA; 466013 MW; 12B85DF96B07B29C CRC64;

Query Match 10.9%; Score 111; DB 2; Length 3896;
Best Local Similarity 25.7%; Pred. No. 1.6e+02;
Matches 45; Conservative 32; Mismatches 68; Indels 30; Gaps 7;

QY 34 KKNQIISYKDIENKV-KSVLYFNRGISDIDLRLSKQAKYTVHFKNGTKRVDL----- 85
Db 3376 KKKKIKNDNDNNINYKELYENNENLALKKQKKQKNNKTKKKKKOMDILYNNDKN 3435
QY 86 KAGIHTADLINTSDIKAISVNVDTKK-----QVXDKKAKANVQVPYITVNGTSQNILSN 140
Db 3436 KKGIN-KKFVNTN--YSININKNNKRFHNIISYKKNKKNVQ-----KNNIKKK 3482
QY 141 LTFKKNQIISYKDLNNVSVLSKNRGIT-----DVDLRLSKQAKFTVNFKNGTKK 191
Db 3483 KTHINKSIVKKNKTNSEISEIKKEHFHQIIEFDSKDKKKKKKKQNVDESSDNKK 3537

RESULT 39
Q8EWV7 PRELIMINARY; PRT; 240 AA.
AC Q8EWV7
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein MYPE920.
GN OrderedLocusNames=MYPE920;
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HP-2;
RX MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL; AP004170; BAC43883.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 240 AA; 27869 MW; 9C98FED493FD003C CRC64;

Query Match 10.9%; Score 110.5; DB 2; Length 240;
Best Local Similarity 24.6%; Pred. No. 7;
Matches 51; Conservative 41; Mismatches 66; Indels 49; Gaps 10;

QY 26 NILSSLTFNRNQI-----SYKDIENKVK-----VLY-----FNRGISDI- 61
Db 8 NMSTASFNKIKQILSNIKQIDSFQDKVNNLSSDNAVIDHFKFRYKNRYRNVVSDFD 67
QY 62 DLRLSKQAKYTVHFKNGTKRVDLKAGIHTADLI-----NTSDIKAISVNVDTKKQ 112
Db 68 DNNLTREKINLNFQKRTERIEDIKKQINFVDYIFSESNNETQASKIKTI-----KGV 121
QY 113 VKDKKAKANVQVPYITVNGTSQNILSNLTFKKNQ-----QISYKDLNNVSVLSKNRGIT 169
Db 122 LSNKEYDLNES-----DINSICDAISNDEGKQELLEELTHKEVSDSTTQDSLSLILT 176
QY 170 -DVDLRLSKQAK-FTVNFKNGTKKVID 194

```


Db 177 QDFLSKLKEGKEISTNFEIKSEKENV D 203

RESULT 40

Q8RBU3 PRELIMINARY; PRT; 398 AA.
AC Q8RBU3;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Predicted transposase.
GN OrderedLocusNames=TTB0715;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013039; AM23977.1; -.
DR InterPro; IPR001959; Transposase_2.
DR InterPro; IPR010095; Tepadset_teng_C.
DR Pfam; PF01385; Transposase_2; 1.
DR Pfam; PF07282; Transposase_35; 1.
DR TIGRFAMs; TIGR01766; tpadset_teng_C; 1.
KW Complete proteome.
SQ SEQUENCE 398 AA; 46552 MW; 6268F889A16A05AE CRC64;

Query Match 10.8%; Score 110; DB 2; Length 398;
Best Local Similarity 24.5%; Pred. No. 13;
Matches 47; Conservative 31; Mismatches 78; Indels 36; Gaps 8;
Qy 21 NGTSNILSSLTFFNQOISYKD-----IENKVSVLYFNRG-ISDIDL 64
Db 116 NGRSVAIFT-----NQCKIKDGHLPFKTNLKLKTRITGKLKEVRIIPKGSVVVIEIV 169
Qy 65 LSKQAKYTVHFKNGTKRVVDLKGAIHT-ADLINTSDIKAISVNDTKQVKDKEAKANVQ 123
Db 170 YEKE---VVETKPKSKRIAGIDLGLNFFVTLVNNIGIRPIVINGKVIKSIHQYNNKKAE 226
Qy 124 VPYTITVNGTSONILSTFKKNQOISYKDLNNVKSVLKSNRGITDVLRLSKQAKFTV 183
Db 227 LMSYVGDGRTS-NRIEKLTLRNNKI--KDLMHKISRFINVWCKQHDID-----TIVI 276
Qy 184 NFKNGTKKVIDL 195
Db 277 GYNSGWKQIEI 288

Search completed: March 16, 2005, 10:39:41
Job time : 177 secs

the Page Blank (uspto)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 10:36:37 ; Search time 41 Seconds
(without alignments)
469.350 Million cell updates/sec

Title: US-10-041-775-2
Perfect score: 1016
Sequence: 1 MRGSHHHHSGSQPYTITV.....FTVNFKNGTKKVIDLKAGIY 200

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	31.3	121	2 S15765	hypothetical prote
2	210	20.7	144	2 F89865	hypothetical prote
3	146.5	14.4	141	2 H90016	hypothetical prote
4	136	13.4	106	2 H89982	truncated map-w pr
5	114.5	11.3	640	2 S33734	DNA topoisomerase
6	114.5	11.3	1272	2 H82926	conserved hypothet
7	112	11.0	1127	2 T28317	ORF MSV156 hypothe
8	112	11.0	4919	2 T31105	hypothetical prote
9	107	10.5	483	2 A69745	hypothetical prote
10	107	10.5	520	2 E97813	WASP, N-WASP, MENA
11	104.5	10.3	297	2 C70231	hypothetical prote
12	103.5	10.2	609	2 S57378	hypothetical prote
13	103.5	10.2	1778	2 AF1116	internalin protein
14	103.5	10.2	3216	2 C90538	hypothetical prote
15	103	10.1	688	2 T43783	hypothetical prote
16	102.5	10.1	410	2 AH1484	probable cell surf
17	102.5	10.1	624	2 PC6003	surface membrane p
18	102.5	10.1	4152	2 T31102	filamentous hemag
19	102	10.0	796	2 T43782	hypothetical prote
20	101	9.9	1536	2 A43855	high-molecular-wei
21	100.5	9.9	405	2 AB1461	B. subtilis yabE p
22	100.5	9.9	450	2 T18440	hypothetical prote
23	100	9.8	451	2 AH1293	hypothetical prote
24	100	9.8	533	2 S52702	REF2 protein - yea
25	99.5	9.8	226	2 E69859	conserved hypothet
26	98.5	9.7	888	2 E82885	hypothetical prote
27	98.5	9.7	1176	2 A33856	surface-layer 125K
28	98	9.6	450	2 E69934	conserved hypothet
29	98	9.6	522	2 D72349	conserved hypothet

30	97.5	9.6	244	2 A86873	transcription regu
31	97.5	9.6	1207	2 S27954	leucine-rich prote
32	97	9.5	647	2 H89988	hypothetical prote
33	97	9.5	3890	2 C89921	hypothetical prote
34	96.5	9.5	408	2 AC1098	B. subtilis yabE p
35	96	9.4	295	2 G97827	hypothetical prote
36	96	9.4	690	2 E84945	glycine-tRNA ligase
37	95.5	9.4	377	2 H82882	hypothetical prote
38	95.5	9.4	521	2 E70129	acid-inducible pro
39	95.5	9.4	682	2 F90603	vipe-like (mycoplas
40	95	9.4	298	2 C97183	probable nucleotid
41	95	9.4	746	2 T47237	myosin II heavy ch
42	95	9.4	1039	2 H95115	conserved hypothet
43	95	9.4	1039	2 D37985	hypothetical prote
44	95	9.4	1398	2 H71606	hypothetical prote
45	94.5	9.3	645	1 SUBSMP	serine proteinase

ALIGNMENTS

RESULT 1

S15765
hypothetical protein 1 (h1b 5' region) - Staphylococcus aureus (fragment)
C:Species: Staphylococcus aureus
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S15765; S04522
R:Projan, S.J.; Kornblum, J.; Kreiswirth, B.; Moghazeh, S.L.; Eisner, W.; Novick, R.P.
Nucleic Acids Res. 17, 3305, 1989
A>Title: Nucleotide sequence: the beta-hemolysin gene of Staphylococcus aureus.
A:Reference number: S15765; MUID:89263748; PMID:2726469
A:Accession: S15765
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-121 <PRO>
A:Cross-references: UNIPROT:P21223; EMBL:X13404; NID:G46586; PIDN:CAA31768.1; PID:G46587

Query Match 31.3%; Score 318; DB 2; Length 121;
Best Local Similarity 76.5%; Pred. No. 5.1e-15;
Matches 62; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY	4	SHHHHHSQIPYITVNGTSQNLSSLTENKQOISYKDIENKVKSVLYFNRGISDIDL 63
Db	41	SLHHGYSKVHPYAITVNGTSQNLSSLTENKQOISYKDIENKVKSVLYFNRGISDIDL 100
QY	64	RLSKQAKYTVHFNGTKRVD 84
Db	101	RLSKQAKYTVHFNGTKKVID 121

RESULT 2

F89865
hypothetical protein SA0841 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89865
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1235-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89865
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <KUR>

A:Cross-references: UNIPROT:Q99VA9; GB:BA000018; PID:G13700785; PIDN:BAB42081.1; GSPDB:
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0841

Query Match 20.7%; Score 210; DB 2; Length 144;
Best Local Similarity 44.3%; Pred. No. 1.2e-07;

Db 637 IYSL-----RNLI-SLTHREYAIYK--HNAWNGFYLNTITSNKDFNLKKNKESY 687
QY 74 HFKN-----GTRKVVLDKAG-----IHTADLINTSDIKAFSVNVDI-----109
Db 688 HLNSLIAHLAIKDEGLKK--DESAGFFLEKLDNDFNLNPKXDEIDVFNVDELDPNLIY 745
QY 110 KQVQKDE--AKANVQVPIYITVNGTSQNLSTFKKQKQIISYKDLNNVKSVLKSNRGI 168
Db 746 ESQVLDKNRRSHVPIPIYSKYI-KKHILEDVEFSLNYALGSEAYENHIYQOIKS----800
QY 169 TDVDLRLSKQAKFTVNFNGTKKVIDLK 196
Db 801 -----QLKPNV-FLNGSKIKVEVK 818
RESULT 7
T28317
ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
C:Species: Melanoplus sanguinipes entomopoxvirus
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T28317
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: Z20484; MUID:99102612; PMID:9847359
A:Accession: T28317
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1127 <AFO>
A:CROSS-references: UNIPROT:Q9YV76; EMBL:AF063866; NID:94049647; PIDN:AAC97677.1; PID:94049647
C:Genetics:
A:Note: MSV156

Query Match 11.0%; Score 112; DB 2; Length 1127;
Best Local Similarity 23.3%; Pred. No. 6.4;
Matches 47; Conservative 40; Mismatches 81; Indels 34; Gaps 9;
QY 20 VNGTSQNLSSITFN-KNQIISYKDIENKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNG 78
Db 177 VSSDEKQLIEQIYKYNINKEIFKNIDNVKEI---NKKQDELNKLDDSKKEFIKKQEE 233
QY 79 TKRVVDLKGAGIHTADLINTSDIKAFSVNVDTKQVKDK-EAKAN-----VQVPIYIT 129
Db 234 LNKTIKK-----QEBLIKLDNKEINFNIDKQKLDQINSKINTLNENIKGMNLYTET 289
QY 130 VNGTSQNLSTFKKQKQIISYKDLNNVKSVL-----LNNVKSVL-----KSNRGITDVLRLSK 177
Db 290 KMKISN-LQNEILNKDSTIKSLDEKQKLDLDELKDNKNNITSLYNKSNKTIINIQOLLES 347
QY 178 QAKFTVNFNGTKKVIDLKAGI 199
Db 348 S---LTFDNANINELKSKI 366

RESULT 8
T31105
hypothetical protein 2 - Haemophilus ducreyi
C:Species: Haemophilus ducreyi
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31105
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A:Reference number: Z20984; MUID:99030326; PMID:9811662
A:Accession: T31105
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4919 <WAR>
A:CROSS-references: UNIPROT:Q9ZHL0; EMBL:AF057696; NID:9329021; PID:g3929023; PIDN:AAC7029023
C:Genetics:
A:Gene: lspa2

Query Match 11.0%; Score 112; DB 2; Length 4919;
Best Local Similarity 25.7%; Pred. No. 38;
Matches 52; Conservative 29; Mismatches 67; Indels 54; Gaps 10;
QY 18 ITVNGTSQ-----NILSSLTENKQKQIISYKDIENKVKSVLYFNRGISDIDL-----RL 65
Db 577 VTLDASKLSANKLDLNVTDNLTNSKSTLSAGELTFFKVKRVNTLNN-----DSELAANNL 632
QY 66 SKQAKYTVHFKNGTKRVVDLKGAGIHTADLINTSDIKAFSVNVDTKQVKDKAKANVQVP 125
Db 633 SLNASHNVTNNKSK-----LSA-----QKADIKAVNLTLNDTTELTAKNLDIN---S 677
QY 126 YTIITVNGTSQNLSTFKK-----NQIISYKDLNNVKSVLKSNRGITD 170
Db 678 TTIITVNGTSQNLSTFKK-----NQIISYKDLNNVKSVLKSNRGITD 170
QY 171 VDLRLSKQAKFTVNFNGTKKVIDLK 192
Db 737 -----FSKNSDFT---SNGSKLV 751

RESULT 9
A69745
hypothetical protein ybbr - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A69745
R:Kumst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C:Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A:Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A:Authors: Schleich, D.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P
Koether, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Mausel
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Krieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, D.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serio
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Yamamoto, H.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69745
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-483 <KUN>
A:CROSS-references: UNIPROT:Q34659; GB:Z99104; GB:Z99105; GB:AL009126; NID:g2632457; PID
A:Experimental source: strain 168
C:Genetics:
A:Gene: ybbr

Query Match 10.5%; Score 107; DB 2; Length 483;
Best Local Similarity 22.4%; Pred. No. 4.9;
Matches 43; Conservative 37; Mismatches 62; Indels 50; Gaps 7;
QY 15 PYITVNGTSQNLSSLTENKQKQIISYKDIENKVKSVLYFNRGISDIDLRLSKQAKYTVH 74
Db 168 PKVQITG-SKNVIDNISLHK-----ASVNLN-----ADETIEKAKVTVY 208
QY 75 FRNGTKRVVDLKGAGIHTADLINTSDIKAFSVNVDTKQVKDKAKANVQ-VPIYITVNGT 133
Db 209 DKDGNALPVDVEPSVITKIVPTVPTSPKVPFKIERTGSLPDGVSITANIESPSSEVTVYG- 267
QY 134 SQNLSTFKKQKQIISYKDLNNVKSVLKSNRGITDVLRLSKQAKET-----VNFKNK 188
Db 268 SQDVLDSLEF-----IDGVSLSLKSINKKDSIEDIADPLPDG 303
QY 189 TKKVIDLKAGIY 200
Db 304 VKKISPSKVTLH 315

Science 294, 849-852, 2001
A;Authors: Kraft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makarewicz, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, W.; Weiss, R.; Zimmermann, S.
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF116
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1778 <GLA>
A;Cross-references: UNIPROT:Q8YA32; GB:NC_003210; PIDN:CAC98412.1; PID:g16409711; GSFPDB:1GZL
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0333

Query Match	10.2%;	Score	103.5;	DB	2;	Length	1778;
Best Local Similarity	20.2%;	Pred. No.	42;				
Matches	50;	Conservative	38;	Mismatches	73;	Indels	87; Gaps 11;
Qy	17	TTITVNGTSONILSLTFKNQOISYKDIEKNVSVLYFNRGISDID	-----	62			
Db	1014	TTVTNKDPAPIISAKT	-----EITYDFKSKTEAAF	-----	DDIDADTNGDSIVTSNFA	1063	
Qy	63	--LRLSKQAKYTVHFKNKGRVVDLKAGIHTADLINTSDIKASVNVDTKKQ	-----	112			
Db	1064	TAVNDKAGDYTVTLNSINS	---DGVAGTPTAIIVHVEKEKIATISNTAQYERYAKIN	1120			
Qy	113	-----VKQKEAKAN	-----VQVP--YTITVNGTSON	-----	136		
Db	1121	ETQFLKDQVHASINASPPTAVLESDFETVVKLDVPQYTVTITATNEDCGVSAPKEVSIV	1180				
Qy	137	-----ILSNLTFKNQOISYKDLNNVKSVLK--SNRGIT	---DVDLRLSKQAKFTV	183			
Db	1181	RKIPAPEITADKEITYPKFDEVSEAEPLNDIHATISDKNVAITSNFSTDVNLKAGDYTV	1240				
Qy	184	NFRKNGTKK	191				
Db	1241	TL-NATNE	1247				

RESULT 14

C90538

hypothetical protein MYPU_2110 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: C90538

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis

A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: C90538

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-3216 <KUR>

A;Cross-references: UNIPROT:Q98QZ9; GB:AL445566; PID:gl4089624; PIDN:CAC13384.1; GSPDB:G

A;Experimental source: strain UAB CTIP

C;Genetics:

A;Gene: MYPU_2110

A;Genetic code: SGC3

	Query Match	10.2%	Score 103.5;	DB 2; Length 3216;
	Best Local Similarity	25.6%;	Pred. No. 86;	
	Matches	50; Conservative	33; Mismatches	83; Indels 29; Gaps 7;
QY	16 YTTVNGTSONILSSITFNKNQQOISYKDIENKYSVL-----YFNRGISDIDLRLSKQA 69	: :	:	:
Dd	201 YEIKV--SSVNVA SLTSNVNLLISRNGIQEKVKYTIIGIIPAYQS KVDANDVRPLKD 258	: :	:	:
QY	70 KYTVHFKNGTKRVVDLKAGHTADLTINTSDIKA --SNVNDTKQVKDKRKANVPVPT 127	: :	:	:
Dd	259 NLVISYNNGIDSPDLINKV--ASQISLND FHP I VPSDNDDYKVVSIRASEQN AQ-SVI 315	: :	:	:
QY	128 ITVNGTSONLSNLTFKKNQOI SYKOLENNKYSVLKS NRGITDV DLRSLSKQAKFTYNFXN 187	: :	:	:

```

Db      316  LTIRKSTKTHGNNA PYSKDYTV EYDNL LSSDMP ELYNNR-----VEANFSVNPQT 365

Qy      188  GTKK-----VIDLK 196
        |      :   ||
        |      :   ||

Db      366  QAKRSAYEYTI SDLK 380

RESULT 15
T43783
hypochemical protein 688 [imported] - slime mold (Dictyostellium discoideum) mitochondrion
C:Species: mitochondrion Dictyostellium discoideum
C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43783
R:Ogawa, S.; Yoshino, R.; Angata, K.; Pi, M.; Iwamoto, M.; Kuroe, K.; Matsuo, K.; Morio,
submitted to the EMBL Data Library, December 1996
A:Description: The Mitochondrial DNA of Dictyostellium discoideum. Complete sequence, ger
A:Reference number: Z22666
A:Accession: T43783
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-688 <OGA>
A:Cross-references: UNIPROT:Q34312; EMBL:AB000109; PIDN:BAA78086.1
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 11
C:Keywords: mitochondrion

```

```

Query Match      10.1%; Score 103; DB 2; Length 688;
Best Local Similarity 24.3%; Pred. No. 14;
Matches 49; Conservative 41; Mismatches 48; Indels 64; Gaps 13;

Qy      26 NILSLTFNKNQQISYKDIENTKVSVLVYNRGI-----SDIDLRLSKQAQKYTVHFKNGT 79
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      518 NVLVSIDSNEVO-----VTNKINYIY--QGILNDKFENKIDLYL--PSGHYFDPGD 567

Qy      80 KRVDVLKAGIHTADLIINT-----SDIKAISNVVDTKQVKQDKEAKANVQVPVITWNGTSQ 135
         :||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      568 REV-----YMTFGQRSEIEKLSSIGNK--IKENSIMGYQLMY----- 605

Qy      136 NILSN--LTFFKNQO----ISKYDLNNVKSVLKSNRGI-----TDVDLRLSKK 178
        |:|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      606 --LNKNWTREKEQDKYLSTREMKEEKRIKVNYLTINNIIENYYMTDIRLSKN 663

Qy      179 AKFTVNFXNGTKVKIDLKAGIY 200

Db      664 LMITGOLRK-EKKI--MEAGIW 682

```

RESULT 16
AH1484
probable cell surface protein (LXPXT motif) [imported] - *Listeria innocua* (strain Clippi1)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1484
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunat, F.; Kurapatk, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1484
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-410 <GLA>
A:Cross-references: UNIPROT:Q92BP3; GB:AL592022; PIDN:CAC95648.1; PTD:gl6412844; GSPDB:C
A:Experimental source: strain Clippi1262
C:Genetics:
A:Gene: lin0415

Query Match	10.1%;	Score 102.5;	DB 2;	Length 410;
Best Local Similarity	21.7%;	Pred. No. 8.1;		

Matches	57; Conservative	35; Mismatches	74; Indels	97; Gaps	13;
QY	23	TSQNILSSLTFN-----	KNQOISYKDIEKVKSVLYFNRGISDIDLRLSKQAK	70	
Db	9	TTVALLSMVVFPIPSMVADAASTSESNLTYKDVNRG-----	FYFGYEDVQLEKGSYK	63	
QY	71	YTVHFK-----	NGTKRW--DLKAGIHTADLINTSDIKAISVNV-DTKKQVKD-----	115	
Db	64	YTVAYEANDMQATNTVTQGSAKAGLF--	IPNSSGVELDSNNVTITQNNVVVDVANDGNK	120	
QY	116	-----	KBKANKV-----QVPYT-----IT-----	VNGT	133
Db	121	VFTHIFEFTVKEDTKADIGTYLGAGSVIPTPDATIIKKNVSVTNETPAEQAEAPVINA	E	180	
QY	134	SQNILSNLFKKNQOISYK-----	DLENNVK-----SVLKSNGRITDVLRLSKQAKFT--	182	
Db	181	DKTIEQNETFDALNEVTATDKXGDLTKSIKVTKNTVDTTKSGEYDVDSYVNSSKLT	TTT	240	
QY	183	-----	VNFKNKGTGKKVIDLK	196	
Db	241	KSVKVTVPVEYKNTAPVIDAK	263		
RESULT 17					
PC6003					
surface membrane protein lmp4 - Mycoplasma hominis (fragment)					
N/Alternate names: hypothetical 624 protein; Lmp4 protein					
C/Species: Mycoplasma hominis					
C/Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004					
C/Accession: PC6003					
R/Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G.					
J. Bacteriol. 178, 2775-2784, 1996					
A/Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene system					
A/Reference number: JC6009; MUID:96213016; PMID:8631664					
A/Accession: PC6003					
A/Molecule type: DNA					
A/Residues: 1-624 <LAD>					
A/Cross-references: UNIPROT:Q49548; EMBL:X95601; NID:g1197335; PIDN:CAA64859.1; PID:g119					
C/Genetics:					
A/Gene: lmp4					
A/Genetic code: SGC3					
C/Superfamily: surface-located membrane protein lmp3; tetratricopeptide repeat homology					
C/Keywords: duplication; membrane protein					
Query Match					
Best Local Similarity					
Matches					
QY	18	ITVNGTS--QNILSSL-----	TFNKNQOISYKDIEKVKSVLYFNRGISD---	60	
Db	307	VASNNATASQSAKSSLDKAVTEITKKLETFNKDKDAKFELSGTRKDIDEFIKQIENDPQ	366		
QY	61	-----	IDRLSLQAKYTVHFKNGTRKRVVD-----	LKAGI-----	89
Db	367	TKKNYQNIQVKNLKDKAENKSITFSNNKKEIQDANKSLQDELNNAKITKKGITDFYNSKK	426		
QY	90	HTADLINTSDIKAISVN-----	VDTKQVKDEKAKANQVPY-TITVNGTSQNILSNLTF	143	
Db	427	QLELDITDADKVGTEADTILDHYKNISD--	ASKNEBIQATQKINDIKKIETKIQE	484	
QY	144	KKNQOIS-YKDLENNVKSVLKSNRGITDV--	DLRLSKQAKFT-VNFKNGTKKKVIDLK	196	
Db	485	KKRENFSEFQIKNELQSFII-NKDLKDQKYSIRTKIENKINGVSSINKNSKIQDIE	540		
RESULT 18					
T31102					
filamentous hemagglutinin 1 - Haemophilus ducreyi					
C/Species: Haemophilus ducreyi					
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004					
C/Accession: T31102					
R/Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.					
J. Bacteriol. 180, 6013-6022, 1998					

A/Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.							
A/Reference number: Z20984; MUID:99030326; PMID:9811662							
A/Accession: T31102							
A/Status: preliminary; translated from GB/EMBL/DBJ							
A/Molecule type: DNA							
A/Residues: 1-4152 <WAR>							
A/Cross-references: UNIPROT:Q9ZHL3; EMBL:AF057695; NID:g3929017; PID:g3929018; PIDN:AAC7							
C/Genetics:							
A/Gene: lspA1							
Query Match							
Best Local Similarity 10.1%; Score 102.5; DB 2; Length 4152;							
Matches 59; Conservative 31; Mismatches 89; Indels 63; Gaps 11;							
QY	10	HGSOIPYITVNGT-----	SON-----	ILSSITFNKNQOISYKDIEKVK	49		
Db	341	YGSNIKFVVTDKGAGVKHKGIIIFSENDINIKMDGNASLKELYAKKDIDIIAKDLIELTEK			400		
QY	50	SVLYFNRI-----	SDIDLR-LSQOAKYTVHFKNGTRKRVVDLKAGIHTADLINTSDIKAI		103		
Db	401	QQLQANNKIILNSTGKINLRNASEVSADNVNVKSENLALENASMSANSLDIVITK---			456		
QY	104	SVNVDTKKQVKDEKAKANVQPYITVNGTS-----	ONILSNLTFKNQOISYKDLF-		155		
Db	457	EVNRSSKVSAGTANIKAS-----	NITLDGSSVVANKITLVNTNNATLNNQSKLSAKDMEL		511		
QY	156	-----	NNVKSVLKSNRGITDVLRLSKQA-----	KFTVN-----	PKNGTKKVIDLKA	197	
Db	512	NVTNITLNTYKSLSAQAQANIKTENLTNGEASLVAEKLDINAIDKITNNGT--			IAGLTA	569	
QY	198	GI	199				
Db	570	NI	571				
RESULT 19							
T43782							
hypothetical protein 796 [imported] - slime mold (Dictyostelium discoideum) mitochondrion							
C/Species: mitochondrion Dictyostelium discoideum							
C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004							
C/Accession: T43782							
R/Ogawa, S.; Yoshino, R.; Angata, K.; Pi, M.; Iwamoto, M.; Kuroe, K.; Matsuo, K.; Morio, K.							
submitted to the EMBL Data Library, December 1996							
A/Description: The mitochondrial DNA of Dictyostelium discoideum. Complete sequence, genomic							
A/Reference number: Z22666							
A/Accession: T43782							
A/Status: preliminary; translated from GB/EMBL/DBJ							
A/Molecule type: DNA							
A/Residues: 1-796 <OGA>							
A/Cross-references: UNIPROT:Q9TGM3; EMBL:AB000109; PIDN:BAA78085.1							
C/Genetics:							
A/Genome: mitochondrion							
C/Keywords: mitochondrion							
Query Match							
Best Local Similarity 10.0%; Score 102; DB 2; Length 796;							
Matches 50; Conservative 30; Mismatches 59; Indels 52; Gaps 11;							
QY	16	YTIIT--VNGTSQNILSSLTFNKNQOISYKDIEKVKSVLYFNRGISDIDLRLSKQ--			AKY	71	
Db	15	YTTTGWVKSTTHGNIINISFNRIQYQROISNKNK-----			NRNLSRVLNLKEKGTARV	69	
QY	72	TVHFKNGTK--RVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDEKAKANVQPYIT				129	
Db	70	TLNKNRKKGRVQVK-----			DILN-----	AKLVQTPVV-	101
QY	130	VNGTSQNILSNLTFKNQOISYKDLLENNVKSVLKSNRGITDV--			DLRLSKQAKFTVNFK	186	
Db	102	-----			BEIKNISFA--SQMVHKE-HDNLPTLRSKQRMLLKAYFDQLRIN-NLKAVNNIF	151	
QY	187	NGTKKVIDLKA				197	
Db	152	TLKKRVNLKS				162	

RESULT 20
A43855
high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae
C:Species: Haemophilus influenzae
C>Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A43855
R:Barenkamp, S.J.; Leininger, E.
A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Haemophilus influenzae serotype 10
A:Reference number: A43855; MUID:92192797; PMID:1548058
A:Accession: A43855
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1536 <BAR>
A:Cross-references: UNIPROT:Q48031; GB:U08876; GB:M84616; NID:G475770; PIDN:AAA20527.1;
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBI:P:89239)

Query Match 9.9%; Score 101; DB 2; Length 1536;
Best Local Similarity 23.9%; Pred. No. 51;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

QY 3 GSHHHHSGQIPYTI-----TVNGTSQNLSSLTFFNQOISYKDIENKVKSV 51
DB 863 GSDFDNH---QKPLTIKKDVIINSGNLTAGGIVNIAGNLTVESN--ANFKAITNFTNV 917
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNKTRVVDLKGAIHTADLIN-TS 98
DB 918 GGLFDNKGNSISIAKGARFKDIDNSKLSITNSSSTYRTII-----SGNITNKG 970
QY 99 DIKAISSVNDTKQ-----VKDKEAKANVQVPYITTVNGTSQNLSSLTFFNQOISYK 152
DB 971 DLNITNEGSDTEMQIGDVSQEG-----NLITSSDKINIKQITIKAGVDGENSDS 1022
QY 153 DLENNVKSVLKSNRGITVDLRLSKQAKYTVHFKNKTRVVDLKGAIHTADLIN-KAG 198
DB 1023 DATNNANLTIKTKEKLTQDLNLSGPNKAEITAKDGS-----DLITG 1064

RESULT 21
AB1461
B. subtilis yabE protein homolog lin0225 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB1461
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, O.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
A:Authors: Krefte, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1461
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <GLA>
A:Cross-references: UNIPROT:Q92P81; GB:AL592022; PIDN:CAC95458.1; PID:gl6412644; GSPDB:G000000000
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0225

Query Match 9.9%; Score 100.5; DB 2; Length 405;
Best Local Similarity 24.4%; Pred. No. 11;
Matches 49; Conservative 32; Mismatches 67; Indels 53; Gaps 10;

QY 11 GSQIPY-----TITVNGTSQNLSSLT-----FNKNQOISYKD-----IENKVKSVL- 52
DB 89 GWEIKYLPARQVTINDNGTKKNVSTKTNVADLLKDNITTPQDVNLVADLTCLKNGLE 148

QY 53 -YFNRGISDIDLRLSKQAKYTVHFKNKTRVVDLKGAIHTADLIN-TS 111
DB 149 VVINRAIE-----LSLQNGTKKDTVTWTTKKVSDLLTEKNIK-----LDKDD 190
QY 112 QV---KDK--EAKANVQVPYITTVNGTSQNLSSLTFFNQOISYKDIENKVKSVLKS 166
DB 191 RVSPKDSNLKERMTVQVTY---VNSKAE-----KKNEQIKFETVYKEDDLSLNGK 239
QY 167 GITDVLRLSKQAKYTVFNKN 187
DB 240 KVVQEGKGEKVEVNVTFEN 260

RESULT 22
T18440
hypothetical protein C0425w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18440
R:Lawson, D.; Bowman, S.; Barrell, B.
A:Reference number: Z18935
A:Reference number: Z18935
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4550 <LAW>
A:Cross-references: UNIPROT:O77336; EMBL:Z98547; NID:e1325376; PID:e1325396; PIDN:CAB111
C:Genetics:
A:Map position: 3
A>Note: C0425w

Query Match 9.9%; Score 100.5; DB 2; Length 4550;
Best Local Similarity 23.6%; Pred. No. 2.1e+02;
Matches 38; Conservative 37; Mismatches 61; Indels 25; Gaps 8;

QY 23 TSQNLSSLTFFNQOISYKDIENKVKSVLYPNRGISDI-DLRLSKQAKYTVHFKNK 81
DB 1362 SSDKITSGISNNMKDINKDKD-KDI-----KNIKDKDKDKDKDKDKDKDKDK 1415
QY 82 VVDLKGAIHTADLIN-TS 125
DB 1416 IKDIKSNEDIKDKVDNDVSSVHLNKCVDNKSQDTQFCPSDDKNINIKKINIKITQ 1475

QY 126 YTTVNGTSQNLSSLTFFNQOISYKDIENKVKSVLKS 165
DB 1476 VYNPLVDSSSSSTDCNKNYKKEK-AVKKIGNIKNIKLN 1515

RESULT 23
AH1293
hypothetical protein lmo1752 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1293
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, O.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
A:Authors: Krefte, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1293
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <GLA>
A:Cross-references: UNIPROT:Q8Y6D5; GB:NC_003210; PIDN:CAC99830.1; PID:gl6411206; GSPDB:G000000000
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1752

Query Match 9.8%; Score 100; DB 2; Length 251;
Best Local Similarity 25.4%; Pred. No. 6.6;

Wed Mar 16 14:08:19 2005

Matches 47; Conservative 32; Mismatches 58; Indels 48; Gaps 11;

QY 17 TITVNG-----TSQNLSSLTFFNKNQOISYKDIE-----KVKSVLYFNRGISDIDLRL 65

Db 77 TIASNGDLLETTNEELKELASSDNR---YKDIKAYRLREAKVSEY---INTKYRY 130

QY 66 -----SKQAKYTVHFKNKGRVVDLKGAGHTADLINTSDIKAISVNVDTKKQVKDEAK 119

Db 131 PTTTIQKFFANVEI--TSGERSVQTEKTPVQIBETTN-NDIK---VSLNTSYSSDDAEVA 184

QY 120 A---NVQVPYITTVNGTSQNILSN-----LTFKKNQOISYKDLNNVKSVLK 163

Db 185 ADIFNSQIPEETITDNTKNLITNKNVTIYPKTFVDFLQKNTWLVFKEQE---EAVIK 241

QY 164 SNRGI 168

Db 242 EPIGI 246

RESULT 24

S52702

REF2 protein - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein YD9346.06; protein YDR195W

C/Species: Saccharomyces cerevisiae

C/Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C/Accession: S52702

R/Oliver, K.; Harris, D.

submitted to the EMBL Data Library, March 1995

A/Reference number: S52697

A/Accession: S52702

A/Molecule type: DNA

A/Residues: 1-533 <OLI>

A/Cross-references: UNIPROT:P42073; EMBL:Z48784; NID:g755782; PID:g755788; MIPS:YDR195W

A/Experimental source: strain AB972

C/Genetics:

A/Genes: SGD:REF2

A/Cross-references: SGD:S0002603; MIPS:YDR195W

A/Map position: 4R

Query Match 9.8%; Score 100; DB 2; Length 533;

Best Local Similarity 25.5%; Pred. No. 16;

Matches 49; Conservative 36; Mismatches 71; Indels 36; Gaps 7;

QY 19 TVNGTSQNILSSLTFFNKNQOISYKDIEKNKSVLYFNRGISDIDLRLSKQAKYTVHFKNK 78

Db 247 TASTSSMKKLKGLFNKNEAKSTESLPTSSKKLSFSKYLKDDADMTKL-----G 297

QY 79 TKRVVDL-----KAGHTADLINTSDIKAISVNVDTKKQVKD---KEAKANVQVPYITIT 129

Db 298 TKRSIDVDFKVNPEASTVSNIISSSTSGSITTVATPASSEPLKTKISVQ----- 351

QY 130 VNGTSQNILSNLTFFKKNQOISYKDLNNVKSULK-----SNRGITVDLRLSKQAKFTV 183

Db 352 -DSNVQSILNRNGPKKARISSIKFLDSDS--QLIKVYGDPLPNQGLQVSTQLKKILK--- 405

QY 184 NFKNGTKKVIDL 195

Db 406 PFKEGEPKEIIL 417

RESULT 25

E69859

conserved hypothetical protein ykoI - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: E69859

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berton

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holbappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Wintere, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: E69859

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-226 <KUN>

A/Cross-references: UNIPROT:O34551; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13184.

A/Experimental source: strain 168

C/Genetics:

A/Genes: ykoI

Query Match 9.8%; Score 99.5; DB 2; Length 226;

Best Local Similarity 23.4%; Pred. No. 6.3;

Matches 50; Conservative 32; Mismatches 69; Indels 63; Gaps 9;

QY 18 ITVNGTSQNILSSLTFFNKNQOISYKDIEKNKSVLYFNRGISDIDLRLSKQAK-YTVHF 76

Db 24 LIIRQTHENVLSKETVVVKVEASY---EGKVTKATQ-----SKDKTYDITL 68

QY 77 NGTKRVVDLKGAGHTADLINTSDIKAISVNVDTKKQVKDEAKANVQVPYITTVNGTSQN 136

Db 69 N-PKGYTFVKADSAIDILSNRVKAVNPSAMTEKEA---EHLALERVPGTVK-KQTRQS 123

QY 137 ILSNLTFFKN-----QQISYKD-----LNNVKSVLKSNRGIT-- 169

Db 124 QVATYTTIQKEDGKTYEVKVDQAKTVLSADQISKQOQKTPITKKEAKTIAERTKGTAD 183

QY 170 -----DVDLRLSKQAKFTVNFKNK 188

Db 184 DADLESEGTLLIFEVDVLDLNDKATVKINAYTG 217

RESULT 26

E82885

hypothetical protein UU481 [imported] - Ureaplasma urealyticum

C/Species: Ureaplasma urealyticum

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C/Accession: E82885

R/Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Caswell, G.H.

submitted to GenBank, February 2000

A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min

A/Reference number: AB2870

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-888 <GLA>

A/Cross-references: GB:AB002145; GB:AF222894; NID:g6899476; PIDN:AAF30893.1; GSPDB:GN001

A/Experimental source: serovar 3; biovar 1

C/Genetics:

A/Genes: UU481

A/Genetic code: SGC3

Query Match 9.7%; Score 98.5; DB 2; Length 888;

Best Local Similarity 21.3%; Pred. No. 39;

Matches 54; Conservative 42; Mismatches 86; Indels 71; Gaps 13;

QY 8 HHGSGQIPYITTVNGTSQNILSSLTFFNKNQOISYKDIE-----KVKSVLYFN---RG 57

Db 547 YNDGDRLVLEVRYNNSTSKESVSLTNKNQEDYSVNIENLTYNREYTLKNIKIHNTNN 606

QY 58 ISDIDLRLSKQAKYTV-----HFKNKT-----KRVVDLKGAGHTAD----- 93

Db 607 ITSIDISKLNKDTFFVVEBSVTKLTFNKNITNDEKFKQIWSRIMEFNI---TNDDEWFSQS 663

QY 94 LINTSDIKAISVNVDTKK-----QVKDKKEAKANVQVPYITTVNGTSQNILSNLTFF--- 143

Db 664 LLNSYKIRAIVENLSTNKNIDDPNIIKIVNDNGPKPQLOI-HINNININDQNEVKLRIVKF 722

QY 144 -KKNQOISYKDYEN-----NVKSVLSNR-----GITDV-----DLRLSKQAKF 181

Db 723 ENKPSYLYKNTINNDWDNIFDYDTNKGVSVIYKSSNTSNVAGIVDIVNDHNIYTTNTSY 782

QY 182 T-VNFKNGTKKVI 193

Db 783 TYVSPSGSVRKLI 795

RESULT 27

A33856

surface-layer 125K protein precursor - Bacillus sphaericus

C:Species: Bacillus sphaericus

C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004

C:Accession: A33856

R:Bowditch, R.D.; Baumann, P.; Yousten, A.A.

J: Bacteriol. 171, 4178-4188, 1989

A:Title: Cloning and sequencing of the gene encoding a 125-kilodalton surface-layer protein of Bacillus sphaericus

A:Reference number: A33856; MUID:89327128; PMID:2666389

A:Accession: A33856

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1176 <BO>

A:Cross-references: UNIPROT:P38537; GB:M28361; NID:g341911; PIDN:AAA50256.1; PID:g556012

F:93-147/Domain: S-layer repeat homology <SLR2>

Query Match 9.7%; Score 98.5; DB 2; Length 1176;

Best Local Similarity 22.4%; Pred. No. 55;

Matches 44; Conservative 33; Mismatches 80; Indels 39; Gaps 7;

QY 20 VNGTSQNLSSITFNKNQOISYKDYENKVSILYFNRGISDID-----LRLSKQAKYT 72

Db 176 IKGSEANGKTNL--NPNAPITRQDF-----AVVFSRTIENDVATPKVDKIEVDAKTLN 227

QY 73 VFHKNGTKRVVDLKGAIHTADLINTSDIKAISVNDVTKKQVKDKAKANVQPYIT--- 129

Db 228 VTLSDGTRKETVTL-----KALEPNKETEVTFKIKDVEYKAKVTYVVTTAT 273

QY 130 -VNGTSQNLSSITFNKNQOISYKDYENKVSILYFNRGISDIDDLRL-SKQAKFTVNFKN 187

Db 274 AVKVSATNLKVVVEFDVTDVKTAEADAANYALKSGTKIKSVLAADNKTATVTLTKL 333

QY 188 GTKK-----VIDLKAG 198

Db 334 NNNKADATISNVKAG 349

RESULT 28

E69934

conserved hypothetical protein ypeB - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: E69934; T44771

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bexter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodura, J.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D., C.M.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Hensaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Laub, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Tognoni, A.; Tosato, V.; Uchiyama, M.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Yata, K.; Yoshida, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: E69934

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-450 <KUN>

A:Cross-references: UNIPROT:P38490; GB:Z99115; GB:Z99116; GB:AL009126; NID:g2634723; PID:g2634723

A:Experimental source: strain 168

R:Moriyama, R.; Hatori, A.; Miyata, S.; Kudoh, S.; Makino, S.

J: Bacteriol. 178, 6059-6063, 1996

A:Title: A gene (sieB) encoding a spore cortex-lytic enzyme from Bacillus subtilis and its role in spore germination

A:Reference number: Z2836; MUID:96427343; PMID:8830707

A:Accession: T44771

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-331 <MOR>

A:Cross-references: EMBL:D79978; NID:g1688021; PIDN:BAAL1474.1; PID:g1688024

A:Experimental source: strain 168

C:Genetics:

A:Gene: ypeB

Query Match 9.6%; Score 98; DB 2; Length 450;

Best Local Similarity 21.5%; Pred. No. 18;

Matches 52; Conservative 40; Mismatches 80; Indels 70; Gaps 11;

QY 8 HHGSGQIPVTITVNGTSQNLSSL-----TFKNQOISY-----KDLE 45

Db 84 HNSVQLPPLTLPFPFNKTEELLSKIGDFSYKTSVRDLQKPLDKNETYSLNKLYQQOSEDIQ 143

QY 46 NKVKSILYF---NRGISDIDLRLS---KQAKYTV--HFKNGTKRVDLKGAIHTADLIN 96

Db 144 NELRHVQHLVMSKNLRWMDVEMALASDEKQSDNTIINSFKTVKKNVGFSTGDLGPSFT 203

QY 97 T-----SOIKALSVNVDTKQVKQKEA-----KANQVQPYITVNGTS 134

Db 204 STKKEEGFSLKKGQISEQEAQIAERFAPDPDNYISIKVKSCKTNRDV-YISMKDPD 262

QY 135 QN--ILSNLTPE-----KNQOISYKDYENKVSILYFNRGISDIDDLRLSKOA 179

Db 263 HKAVIYMDITKGGHPVYLIQNRVKDOKISLNDGNSRALAFKKNGFETD-DLEIDES 321

QY 180 KF 181

Db 322 QY 323

RESULT 29

D72349

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: D72349

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D., C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing of Thermotoga maritima

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: D72349

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-522 <ARN>

A:Cross-references: UNIPROT:Q9WZD1; GB:AE001739; GB:AE000512; NID:g4981176; PIDN:AAD3574

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0663

C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0466

Query Match 9.6%; Score 98; DB 2; Length 522;

Best Local Similarity 19.8%; Pred. No. 22;

Matches 46; Conservative 43; Mismatches 67; Indels 76; Gaps 9;

QY 4 SHHHHH-----GSQIPYIT-----VNGTSQNLSSITFNKNQOISYKDLEN 46

Db 90 SHAHADTGMVGLIDEXIDELPLLMGTETFAVRCASVTYSNVLTLGGKKRRKNDKLEN 149

QY 47 KVSILYFNRGISDIDLRLSKQAKYTVHFK-NGTKRVVDLK----- 86

A:Cross-references: UNIPROT:Q99UE3; GB:BA000018; PID:g13701233; PIDN:BAB42528.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: ebhB

Query Match 9.5%; Score 97; DB 2; Length 3890;
Best Local Similarity 21.4%; Pred. No. 3e+02;
Matches 49; Conservative 31; Mismatches 73; Indels 76; Gaps 9;

QY 17 TITVNGTSQNILSLTFNKNQOISYKDIENKVKSVLYFNRG--ISDIDLRLSKQAKYTVH 74
Db 1036 TAVSNDKQSIITAF-MNKNQMI-----RGYLASTDPVTVDNNGNVTLH 1078
QY 75 FNGTKRVVD-----LKAGIHTADLINTSDI---KALSUNVDTTKQVKDEKAKAN 121
Db 1079 YRDGSSLTLDATNVMTYEPVVKSEYQTANAATATVTIAKGOSFNTGDIKQY----- 1130
QY 122 VQVPYVIT-----VNGTSQNILSLTFNKNQOISYKDIENKVKSVLKSNNR----- 166
Db 1131 ----FTLSNGQALPNGTFTNITSRTIPTAQEVSQNNAGTQLVHIVASNAHYKDTEDFYI 1186
QY 167 --GITDV-----DLRLSKQAKFTVNFNKGTKKVIDLKA 198
Db 1187 SLKIVDVKQPEGQVRVTRSTYDLTDTDEISKVKQAFINARDVITLAE 1235

RESULT 34
AC1098
B. subtilis YabE protein homolog lmo0186 [imported] - Listeria monocytogenes (strain EGD
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1098
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Sincos, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1098
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-408 <GLA>
A:Cross-references: UNIPROT:Q8YAB4; GB:NC_003210; PIDN:CAC98401.1; PID:g16409543; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0186

Query Match 9.5%; Score 96.5; DB 2; Length 408;
Best Local Similarity 24.2%; Pred. No. 21;
Matches 50; Conservative 34; Mismatches 74; Indels 49; Gaps 10;

QY 11 GSOIIPV-----TITVNGTSQNILSS-----LTFNKN-----QQISYKDIENKVKSVL- 52
Db 89 GMEIKLPARQITINDNGTKDQVSWTKYANVALLDENTTPRPQVNLVALDTKNGLUE 148
QY 53 -YFNRGISDIDLRLSKQAKYTVHFNKGTRVVDLKAIGIHTADLINTSDIKAISVNVDTKK 111
Db 149 VNINRAI-----QLSLQ-----NGAKKDTVTITTKVSDLLAEKNIK-----LDQDD 190
QY 112 QV---KDEKAKANVQVPTITVNGTSQNILSLTFNKNQOISYKDIENKVKSVLKSNNRGI 168
Db 191 RVSPAKDSNLKRMVTEVTVY-VNSKAE-----KKNEQVKFETVYKEDDLSLNKGVEKV 241
QY 169 TDVDLRLSKQAKFTVNFNKGTKKVIDL 195
Db 242 VOEGKNGKKVVEYKVTTFENGKKKRDV 268

RESULT 35
G97827
hypothetical protein RC1023 [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97827
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ri
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: G97827
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <KUR>
A:Cross-references: UNIPROT:Q92GU9; GB:AE006914; PIDN:AAL03561.1; PID:g15620140; GSPDB:
C:Genetics:
A:Gene: RC1023

Query Match 9.4%; Score 96; DB 2; Length 295;
Best Local Similarity 23.3%; Pred. No. 15;
Matches 49; Conservative 36; Mismatches 65; Indels 60; Gaps 10;

QY 10 HGSQIIPV--TITVNGTS-----QNILSSLTFNKNQOISYKDIENKVKSVLYFNR 56
Db 105 HGSLLQYLKRSVNPDSFISQIKSELIKMNLSSL--SRSVQVSNKEID-----VAILSS 157
QY 57 GISDIDLRL-----SKQAKYTVHFNKGTRVVDLKAIGIHTADLINTSDIKAISVNV 107
Db 158 DQKVEISMQVFTSKDGGNKAPTQNNLNKRLKCADVK-----KSLYDNF 203
QY 108 DTKQVKDKKAKANVQVPTITVNGTSQNILSLTFNKNQOISYKDIENKVKSVLKSNNR 167
Db 204 ATMQIITDKLSK-----IEGVKQTIKDLTPDKASNVF--EVNNKFEITLVCSSK 251
QY 168 ITDVLRLSKQAKFTVNFNKGTKKVIDLKA 197
Db 252 ILNVN---EDENNVYVNFEL--TNKKISQKA 276

RESULT 36
E84945
glycine-tRNA ligase (EC 6.1.1.14) beta chain [imported] - Buchnera sp. (strain APS)
N:Alternate names: glycyl-tRNA synthetase beta chain
C:Species: Buchnera sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 03-Jun-2002
C:Accession: E84945
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: E84945
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-690 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: glys; BUI35
A:Superfamily: glycine-tRNA ligase beta chain
C:Keywords: ligase

Query Match 9.4%; Score 96; DB 2; Length 690;
Best Local Similarity 21.7%; Pred. No. 42;
Matches 55; Conservative 35; Mismatches 54; Indels 110; Gaps 12;

QY 22 QTSQ---NILS--SLTFNKN-----QQISYKDIENKVKSVLYFNR-----GISDIDL 63
Db 11 GTEELPARLLSKISLYFYKKNFKIKELDFHNISYKNIK-----YFSTPRRLALKIKIDI 63
QY 64 RLKSKQAKYTVHFNKGTRVVDLKAIGIHTADLINTSD-----IKAISVNVV---- 108
Db 64 -----TERFVEIKK--RGFSINSYDKDGFLEATAATRLKHGGINQAI 106
QY 109 -----TKKQVKDKE-----AKANVQVPTI----- 128
Db 107 RLKNEKGWLFYKTRKKKNIESLIPKITESALKNISIKKSNRWQDNQKFSRPIRNI 166

QY 129 -----TVNGTSQNLSTFKKQKQISYKDLNNVKSVLKSNRGITVDVLRSLKQ 178
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 167 LLDKKVIPGDVFNITSKNLLQHLSSKQSIKIDAKDYPKILLERKNIADYPIR---K 223
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 179 AKFTVNFKNQKTKV 192
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 224 EKIIEDIENIAKKI 237
| | | | | : | | | | : | | | | : | | | | : | | | | :
RESULT 37
H82882
hypothetical protein UU497 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: H82882
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
A:Reference number: A82870
A:Accession: H82882
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <GLA>
A:Cross-references: GB:AE002148; GB:AF222894; NID:G6899495; PIDN:AAF30909.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UU497
A:Genetic code: SGC3
Query Match 9.4%; Score 95.5; DB 2; Length 377;
Best Local Similarity 24.3%; Pred. No. 22;
Matches 54; Conservative 30; Mismatches 75; Indels 63; Gaps 12;
QY 22 GTSNILSLTFKNK-QQISYKDIEKNKSVLY-----FNRGISDIDLRLSKQAKYTVHFK 76
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 85 GNKINVDINPEYKNLQMLSPK-LENLKPNTTYKITKFNITGHEVDLQTQKDSLFTTKAE 143
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 77 NGTKRVVDLKAGIHTADLINTSDIKAI SVNVDTKKQVKDKAKANVQVYTTIVNGTSON 136
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 144 NLLPDIPNLPNSVG-----TEIKDIKTNSLSDA-----TKVNVNVNLEIN-QSTLEN 190
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 137 ILSNLTFFKNQKQISYKDLNNVK-SVLKSNRGITD-----VDLRLSK 177
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 191 QVARLYKSDN-SWK-LSNTLKIAEIKNSFVLGDLISNRKYLKELIIGSQSDNLNTN 248
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 178 -QAKFTVN-----FKNGTKKVIDLK 196
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 249 AQTKITTNLSLPTTAPKPEIKSVLIDTKFDNHPSSLNLK 290
| | | | | : | | | | : | | | | : | | | | : | | | | :
RESULT 38
E70129
acid-inducible protein (act206) homolog - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: E70129
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: E70129
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-521 <KLE>
A:Cross-references: UNIPROT:O51253; GB:AE001134; GB:AE000783; NID:G2688133; PIDN:AAAC6663
A:Experimental source: strain B31
C:Superfamily: apolipoprotein N-acyltransferase
Query Match 9.4%; Score 95.5; DB 2; Length 521;

Best Local Similarity 21.4%; Pred. No. 32;
Matches 52; Conservative 35; Mismatches 77; Indels 79; Gaps 10;
QY 14 IPTTIV-----NGTSQNLSSLTF-----KKNQQIS 40
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 91 IPYSLTLGYFLYSLKSFKNKMSITMLFTFYDSRSIGFLAYPWGLAAFTVNNFNLIQ 150
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 41 YKDIEKN--VKSVLVF-NRGISDIDLRLSK-----QAKYTVHFKNGTKRVVDLKAG 88
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 151 IADIFGVFFSVFVFLNSGIADFLIHKNTLLNTAFLLITASTFTYGMICKIELKNL 210
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 89 IHTADLINTSDIKAISVNVVD-----TKQVKD-----KEAKNVQVPTTIVNGTSON 136
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 211 L--AKEIDSLNIAAIQLNTDPLPGNDKKGIRDSIBITEQALKENPKIEFV-----WSEG 264
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 137 ILSNLTFFKNQKQISYKDLNNVKSVLKSNRGITVDLRLSKQAKFTVNFKNQKTKKVIDLK 196
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 265 VLTYPFSKEDQHPKSSDLHNLKNFIKEHK-----IPFAIGAPSNLDKA 308
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 197 AGI 199
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 309 IGI 311
| | | | | : | | | | : | | | | : | | | | : | | | | :
RESULT 39
F90603
vlpE-like (mycoplasma hyorhinis) lipoprotein [imported] - Mycoplasma pulmonis (strain UA
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: F90603
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Sanson, D.; Gallison, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: F90603
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-682 <KUR>
A:Cross-references: UNIPROT:Q98P18; GB:AL445566; PID:gl4090149; PIDN:CAC13907.1; GSPDB:G
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 7340
A:Genetic code: SGC3
Query Match 9.4%; Score 95.5; DB 2; Length 682;
Best Local Similarity 20.5%; Pred. No. 45;
Matches 54; Conservative 39; Mismatches 55; Indels 115; Gaps 12;
QY 16 YTTIVNGT-----SQNTLSLTFN-----KNQQISYKDIEKNKSVLYFNRG-- 57
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 294 YTPTLDGSDYKSFEEYNRIKEILTSLNFSVKBEKHILSFSEKSS-----DFNLGLL 348
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 58 -----ISDIDLRLS-----KOAKYTVHFKN----- 77
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 349 AKEGNDVGFPPKTELESKEISDIDMQITFSPKDDAVGEKNGKFKIEFLAQSLLFETIE 408
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 78 -----GTRKVVLD-----KAGIHTADLINTSDIKAISVNV 107
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 409 KNIEWKYKTAEKIMEDFAKGERVTELENLYNHFKDKANIHPPML-----KDLTTNV 462
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 108 DTKQVKQDKEAKANVQVYTTIVNGTSON1-----LSNLTFFKNQKQISYKDLNNVKSVL 162
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 463 D-GKQVKTADNKINLKGQVATLKG-SKGVNDYQGSATLIFEVDYRGSKQKQVEITINDFA 520
| | | | | : | | | | : | | | | : | | | | : | | | | :
QY 163 K-----SNRGITDVLRLS 176
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 521 KVAPHEENVGKNRLQDFDIRAS 543
| | | | | : | | | | : | | | | : | | | | : | | | | :
RESULT 40
C97183
probable nucleotidyltransferase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum

Search completed: March 16, 2005, 10:43:23
Job time : 45 secs

1111 Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 10:42:42 ; Search time 137 Seconds
(without alignments)
482.542 Million cell updates/sec

Title: US-10-041-775-2

Perfect score: 1016

Sequence: 1 MRGSHHHHHSQIPYITIV.....FTVNFNGTKVKVIDLKAGIY 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1401741 seqs, 330541175 residues

Total number of hits satisfying chosen parameters: 1401741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1016	100.0	200	14	US-10-041-775-2
2	626	61.6	131	9	US-09-982-992A-2
3	626	61.6	131	14	US-10-041-775-4
4	440	43.3	150	8	US-08-781-986A-5238
5	440	43.3	150	15	US-10-329-624-5238
6	210	20.7	151	8	US-08-781-986A-5233
7	210	20.7	151	15	US-10-329-624-5233
8	142	14.0	141	17	US-10-470-048B-221
9	133	13.1	343	15	US-10-378-674-4
10	131	12.9	316	15	US-10-378-674-6
11	117.5	11.6	391	14	US-10-057-531A-7
12	117.5	11.6	391	14	US-10-057-532A-7
13	116.5	11.5	512	9	US-09-813-820-6
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 4, Appli
					Sequence 5238, Ap
					Sequence 5238, Ap
					Sequence 5233, Ap
					Sequence 5233, Ap
					Sequence 221, App
					Sequence 4, Appli
					Sequence 6, Appli
					Sequence 7, Appli
					Sequence 6, Appli

14	115	11.3	374	15	US-10-282-122A-72043	Sequence 72043, A
15	114.5	11.3	393	14	US-10-057-531A-3	Sequence 3, Appli
16	114.5	11.3	393	14	US-10-057-532A-3	Sequence 3, Appli
17	114	11.2	211	9	US-09-813-820-4	Sequence 4, Appli
18	113.5	11.2	246	15	US-10-282-122A-53616	Sequence 53616, A
19	111	10.9	963	15	US-10-282-122A-61097	Sequence 61097, A
20	110	10.8	1220	14	US-10-193-764-28	Sequence 28, Appli
21	110	10.8	1226	14	US-10-193-764-26	Sequence 26, Appli
22	108.5	10.7	371	15	US-10-404-667-5	Sequence 5, Appli
23	106	10.4	345	9	US-09-813-820-7	Sequence 7, Appli
24	105	10.3	560	15	US-10-378-674-2	Sequence 2, Appli
25	104	10.2	159	9	US-09-813-820-2	Sequence 2, Appli
26	104	10.2	1051	15	US-10-282-122A-70558	Sequence 70558, A
27	103.5	10.2	609	15	US-10-369-493-2021	Sequence 2021, Ap
28	103.5	10.2	1778	15	US-10-282-122A-60961	Sequence 60961, A
29	102.5	10.1	184	10	US-09-345-373-30	Sequence 30, Appli
30	102.5	10.1	184	14	US-10-075-446-30	Sequence 30, Appli
31	102.5	10.1	184	14	US-10-035-212-30	Sequence 30, Appli
32	102.5	10.1	184	17	US-10-901-210-30	Sequence 30, Appli
33	101.5	10.0	371	15	US-10-404-667-2	Sequence 2, Appli
34	101.5	10.0	775	16	US-10-437-963-179404	Sequence 179404,
35	101.5	10.0	3241	9	US-09-841-786-1	Sequence 1, Appli
36	101.5	10.0	3241	15	US-10-647-057-1	Sequence 1, Appli
37	101	9.9	1095	14	US-10-193-764-65	Sequence 65, Appli
38	101	9.9	1536	13	US-10-052-880-2	Sequence 2, Appli
39	101	9.9	1536	14	US-10-193-764-63	Sequence 63, Appli
40	101	9.9	1536	17	US-10-681-171-2	Sequence 2, Appli
41	100	9.8	262	9	US-09-895-828-457	Sequence 457, App
42	100	9.8	262	14	US-10-114-666-457	Sequence 457, App
43	100	9.8	533	16	US-10-477-369-47	Sequence 47, Appli
44	99.5	9.8	177	17	US-10-842-989-27	Sequence 27, Appli
45	99.5	9.8	330	14	US-10-279-793-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-10-041-775-2

; Sequence 2, Application US/10041775

; Publication No. US20030108564A1

; GENERAL INFORMATION:

; APPLICANT: BROWN, Eric L.

; APPLICANT: LEE, Lawrence

; APPLICANT: HOOK, Magnus

; TITLE OF INVENTION: METHOD OF PREVENTING T CELL-MEDIATED RESPONSES BY THE USE OF TH-

; TITLE OF INVENTION: HISTOCOMPATIBILITY COMPLEX CLASS II ANALOG PROTEIN (MAP PROTEIN)

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS

; FILE REFERENCE: P07023US01/BAS

; CURRENT APPLICATION NUMBER: US/10/041,775

; CURRENT FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: 60/260,523

; PRIOR FILING DATE: 2001-01-10

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 200

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-10-041-775-2

Query Match	100.0%;	Score	1016;	DB	14;	Length	200;
Best Local Similarity	100.0%;	Pred. No.	1.7e-71;				
Matches	200;	Conservative	0;	Mismatches	0;	Indels	0;
		Gaps	0;				
Qy	1	MRGSHHHHHSQIPYITIVNGTSONILSSLTFNKNQOISYKDIENKVKSVLYFNRGISD	60				
Db	1	MRGSHHHHHSQIPYITIVNGTSONILSSLTFNKNQOISYKDIENKVKSVLYFNRGISD	60				
Qy	61	IDRLRSKQAKTVHFKNGTKRWVDLKAGIHTADLINTSDIKAKISVNVDTKKQVKDKAKA	120				
Db	61	IDRLRSKQAKTVHFKNGTKRWVDLKAGIHTADLINTSDIKAKISVNVDTKKQVKDKAKA	120				

QY 121 NVQVPYITVNGTSQNILSLTFKKNQOISYKDLNNVSVLKNRGIITDVLRLSKQAK 180
Db 121 NVQVPYITVNGTSQNILSLTFKKNQOISYKDLNNVSVLKNRGIITDVLRLSKQAK 180
QY 181 FTVNFKNGTKKVIDLKAGIY 200
Db 181 FTVNFKNGTKKVIDLKAGIY 200

RESULT 2

US-09-982-992A-2
; Sequence 2, Application US/09982992A
; Patent No. US20020164337A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M. et al.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE MAP PROTEIN AND METHOD OF USE IN TRE
; FILE REFERENCE: P06922US02/BAS
; CURRENT APPLICATION NUMBER: US/09/982,992A
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/277,287
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/241,832
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-982-992A-2

Query Match 61.6%; Score 626; DB 9; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSHHHHGSQIPYITVNGTSQNILSLTFKKNQOISYKDLENKVSVLVFNRGISD 60
Db 1 MRGSHHHHGSQIPYITVNGTSQNILSLTFKKNQOISYKDLENKVSVLVFNRGISD 60
QY 61 IDRLSKQAKYTVHFKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
Db 61 IDRLSKQAKYTVHFKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120

QY 121 NV 122
Db 121 NV 122

RESULT 3

US-10-041-775-4
; Sequence 4, Application US/10041775
; Publication No. US20030108564A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, Eric L.
; APPLICANT: LEE, Lawrence
; APPLICANT: HOOK, Magnus
; TITLE OF INVENTION: METHOD OF PREVENTING T CELL-MEDIATED RESPONSES BY THE USE OF THE
; TITLE OF INVENTION: HISTOCOMPATIBILITY COMPLEX CLASS II ANALOG PROTEIN (MAP PROTEIN)
; FILE REFERENCE: P07023US01/BAS
; CURRENT APPLICATION NUMBER: US/10/041,775
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/260,523
; PRIOR FILING DATE: 2001-01-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-041-775-4

Query Match 61.6%; Score 626; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGSHHHHGSQIPYITVNGTSQNILSLTFKKNQOISYKDLENKVSVLVFNRGISD 60
Db 1 MRGSHHHHGSQIPYITVNGTSQNILSLTFKKNQOISYKDLENKVSVLVFNRGISD 60
QY 61 IDRLSKQAKYTVHFKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
Db 61 IDRLSKQAKYTVHFKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
QY 121 NV 122
Db 121 NV 122

RESULT 4

US-08-781-986A-5238
; Sequence 5238, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5238

Query Match 43.3%; Score 440; DB 8; Length 150;
Best Local Similarity 78.9%; Pred. No. 8.5e-27;
Matches 86; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 4 SHHHHHGSQIPYITVNGTSQNILSLTFKKNQOISYKDLENKVSVLVFNRGISD 63
Db 42 SLHHGSKVHVFPYAITVNGTSQNILSLTFKKNQOISYKDLNKKVLSKSDRGISD 101
QY 64 RLSQAKYTVHFKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 112
Db 102 RLSQAKYTVHFKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 150

```
RESULT 5
US-10-329-624-5238
; Sequence 5238, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;   Gil H. Choi
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5233
; Query Match 20.7%; Score 210; DB 8; Length 151;
; Best Local Similarity 44.3%; Pred. No. 7.1e-09;
; Matches 43; Conservative 22; Mismatches 32; Indels 0; Gaps 0;
QY 14 IPYTTVNGTSQNILSSLTFFNKNQOISYKDIENKVKSVLYFNRGISDIDLRLSKQAKYTV 73
Db 55 VPTYIADVGINAFNQSGLNLPKDSQSLSYLDLGNKVKALLYDGRGVTPEKIRNAKSAVYTI 114
QY 74 HFKNQTKRVLDLKAGIHTADLINTSDIKAISVNVDTK 110
Db 115 TWKDGSKKEVDLKKDSYTANLFDNSIKQIDINVTK 151
RESULT 6
US-10-329-624-5238
; Sequence 5233, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248PDI1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5238:
US-10-329-624-5238
Query Match 43.3%; Score 440; DB 15; Length 150;
Best Local Similarity 78.9%; Pred. No. 8.5e-27;
Matches 86; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
QY 4 SHHHHSGSQPYTTVNGTSQNILSSLTFFNKNQOISYKDIENKVKSVLYFNRGISDIDL 63
Db 42 SLHGGYKVPYVAYTAVNGTSQNILSSLTFFNKNQOISYKDIENKVKSVLKSDDRGISDIDL 101
QY 64 RLSQAKYTVHFKNGTKVVDLKAGIHTADLINTSDIKAISVNVDTKKQ 112
Db 102 RLSQAKYTVVFPNGTKKVIDLKAGIYTDLINTSEIKAININVDTKKQ 150
RESULT 7
US-10-329-624-5233
; Sequence 5233, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
;   Gil H. Choi
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
```

Wed Mar 16 14:08:18 2005

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5233:
US-10-329-624-5233

Query Match 20.7%; Score 210; DB 15; Length 151;
Best Local Similarity 44.3%; Pred. No. 7.1e-09;
Matches 43; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

Qy 14 IPYITVNGTSONILSSITFNKQOISYKDIENKVKSVLYFNRGISDIDLRLSKQAKYTV 73
Db 55 VPYITADGIMAFNOSYLNLPKDSQSLYDLGNKVALYDERGVTPKIRNAKSAVYTI 114

Qy 74 HFKNGTKRVVDLKGAGIHTADLINTSDIKAISVNVDTK 110
Db 115 TWKDSKKEVDLKKDSYANLPFDSNSIKQIDINVTK 151

RESULT 8
US-10-470-048B-221
; Sequence 221, Application US/10470048B
; Publication No. US20050037444A1
; GENERAL INFORMATION:
; APPLICANT: MEINKE ET AL.
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
; FILE REFERENCE: SONN:035US
; CURRENT APPLICATION NUMBER: US/10/470,048B
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 221
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-470-048B-221

Query Match 14.0%; Score 142; DB 17; Length 141;
Best Local Similarity 33.0%; Pred. No. 0.0013;
Matches 31; Conservative 25; Mismatches 38; Indels 0; Gaps 0;

Qy 14 IPYITVNGTSONILSSITFNKQOISYKDIENKVKSVLYFNRGISDIDLRLSKQAKYTV 73
Db 47 VPYITSDGITALHRTYFIFPENKNVLYQEIDSKVKNELASQRGVTTKINNAQTATYTL 106

Qy 74 HFKNGTKRVVDLKGAGIHTADLINTSDIKAISVNV 107
Db 107 TLNDGNKKVNVLLKNDDAKNSIDPSTIKQIQIVV 140

RESULT 9
```

```

US-10-378-674-4
; Sequence 4, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI
; FILE REFERENCE: P07556US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-4

Query Match 13.1%; Score 133; DB 15; Length 343;
Best Local Similarity 22.4%; Pred. No. 0.02;
Matches 54; Conservative 32; Mismatches 71; Indels 84; Gaps 9;

Qy 1 MRGSHHHHHGSGQIP-----YITVNGTS-----QNILSSLTFF 33
Db 1 MRGSHHHHHGSLVPRGSEQGSNVNHLIKVTQDSITEGYDDSDGIKAHAENLIYDVTF 60

Qy 34 NKQOISYKDIENKVK-----VLYFNRGISDIDL-----RLS 66
Db 61 -----EVDDKVKSGDWTWNIDKNVTSPDUTDSFAIPKIDNKGSEIATGYDNTN 111

Qy 67 KQAKYTVHFNGTKRVVDLKGAGIHTADLINTSDIKAISVNVDTKKQVKDKREKANVQVPY 126
Db 112 KQIYTV--FDYVDKYENIKAKHLKLTYSIDKSKVP-----NNNTKLDVEYKTALSSVNKTI 165

Qy 127 TITVNGTSQNILSNLTF-----KKNQOIS-----YKLENNVKSVLKSNRGITDV 171
Db 166 TVEYQKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRSAKETNVNISGNGDEGSTII 225

Qy 172 D 172
Db 226 D 226

RESULT 10
US-10-378-674-6
; Sequence 6, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI
; FILE REFERENCE: P07556US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-6

Query Match 12.9%; Score 131; DB 15; Length 316;
Best Local Similarity 22.6%; Pred. No. 0.025; 71; Indels 78; Gaps 9;
Matches 53; Conservative 33; Mismatches 71; Indels 78; Gaps 9;

Qy 1 MRGSHHHHHGSGQ-----IPYITVNGTS-----QNILSSLTFFNKQOI 39
Db 1 MRGSHHHHHHSGEQGSNVNHLIKVTQDSITEGYDDSDGIKAHAENLIYDVTF----- 54
```



```

; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-813-820-6

Query Match      11.5%; Score 116.5; DB 9; Length 512;
Best Local Similarity 23.8%; Pred. No. 0.63; Indels 97; Gaps 14;
Matches 64; Conservative 29; Mismatches 79;

QY 1 MRGSHHHHHSQIPYITVNGTSQNLSS-----LTF-NKNOQISYKD----- 43
Db 1 MRGSHHHHHSQIPYITVNGTSQNLSS-----LTF-NKNOQISYKD----- 43
QY 44 -----IENKVS-----LYFN-----RGISDIDRLSKQAKYT 72
Db 60 WPTSGTVKIEGYSKTVPLTVKGEQVQAVITPDGATITFNDKVEKLSV-----SGFAEFE 115
QY 73 VHFKNQTKRVVDLKGAGHTADLINTSDIKAISV---NVDTKQVQKDKA----- 118
Db 116 VQGRNLQ-----TNTSDDKVATITSGNSTVTVHKSEAGTSSVFFYKGTG 161
QY 119 -----KANQVQVYITVNGTSQNLSTFKK-----NQGISYKDLNNV-----KSVLKNR 166
Db 162 DMLPEDTTHVRWFLNNEKSYSVKDITIKQIQGGQQLDLSTLNTVNGTSHSNYSQGS 221
QY 167 GITVDVLRSLKQAKFTVAFKNGTKKVIDL 195
Db 222 AITDFE-KAFPGSKITV---DNTKNTIDV 246

RESULT 14
US-10-282-122A-72043
; Sequence 72043, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Cart, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72043
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-282-122A-72043

Query Match      11.3%; Score 115; DB 15; Length 374;
Best Local Similarity 24.2%; Pred. No. 0.55; Indels 58; Gaps 13;
Matches 52; Conservative 42; Mismatches 63;

QY 18 ITVNGTSQNLSSITFNKNQOISYKDIENKVSIVY----FNRGISDIDRLSKQAKYTV 73
Db 131 ITVSGNKNAIESQLI----BELGIKK-SDYLTTLFQANRPERNLKSKD-KWVKEAKLVY 184
QY 74 HFKNG-TKRVVD-----LKGAGHTADLINTSDIKA--ISVNVDTKKQVK 114
Db 185 HFPNHFTLRVKEYRIIAYRQTDKGYVPLENGTR-VDTVANASELPGSFVTINLDOEKEVR 243
QY 115 -----DKEAKANVQVYITVNGTSQNLSTFKKNQOISYKDLNNKSVLKS 165
Db 244 ELVOKLAKLKLKSLVGSIRV--ISSVNSSTYKDLLEKKN-----NSVRVPL---- 289
QY 166 RGITVDVLRSLKQAKFTVFNKNGTKKVIDLKAGIY 200
Db 290 ---SEIDTKLPYYSKIKKNTLDGS--IVDMEVGIV 319

RESULT 15
US-10-057-531A-3
; Sequence 3, Application US/10057531A
; Publication No. US20030161838A1
; GENERAL INFORMATION:
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite
; TITLE OF INVENTION: Protein-142 Vaccine
; FILE REFERENCE: 003/241/SAP
; CURRENT APPLICATION NUMBER: US/10/057,531A
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/264,535
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/347,564
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 3
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein
; OTHER INFORMATION: Sequence in pET42A
US-10-057-531A-3

Query Match      11.3%; Score 114.5; DB 14; Length 393;
Best Local Similarity 22.5%; Pred. No. 0.64;
Matches 53; Conservative 34; Mismatches 90; Indels 59; Gaps 10;

QY 4 SHHHHHH-GSQIP--YITVNGTSQNLSSITFNKNQOISY-----KDIENKV 48
Db 2 AHHHHHPGSGIEGRGTMAISVTMDNILSG--FENEYDVLYLKLPLAGVYSLKKQIE--- 56
QY 49 KSVLYFNRGISDIDRLSKQAKYTVHFKNGTKRVVDLKGAGHTADLINTSDIKAISVND 108
Db 57 KNITFTNLNLDILNSRLKRRKRYL-----DVLESOLMFKHSSNEYIIE 102
```

QY 109 TKKQVKDEKAKANVQPTITVNGTSQNT---LSNLTFFKKNQOISYKDLNNVSKVLKSN 165
Db 103 DSFKLLNSQKNTLLKSYKIKESVENDIKFAQEGISYKVKYKDLKSLKIKKVKIEE 162
QY 166 R-----GITDVLRLSKQAKFTVN---FKNGTKKV-----IDLKAGI 199
Db 163 KEKFPSSPPTTPPSAKTDEQKESKFLPFLNIETLYNNLVNKIDDDYLINLKAKI 218

RESULT 16
US-10-057-532A-3
; Sequence 3, Application US/10057532A
; Publication No. US20030161839A1
; GENERAL INFORMATION:
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Cohen, Evelina
; APPLICANT: Cohen, Joe D.
; APPLICANT: Voss, Gerald
; TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine
; FILE REFERENCE: 003/238/SAP
; CURRENT APPLICATION NUMBER: US/10/057,532A
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/264,535
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/347,564
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 3
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein Sequence in
US-10-057-532A-3

Query Match 11.3%; Score 114.5; DB 14; Length 393;
Best Local Similarity 22.5%; Pred. No. 0.64;
Matches 53; Conservative 34; Mismatches 90; Indels 59; Gaps 10;

QY 4 SHHHHH-GSQIP--YTIIVNGTSQNLSSLLFNKNQIQSY-----KDIENKV 48
Db 2 AHHHHHPGSGEGRTMAISVTMNLISG--FENEYDVIYKPLAGVRSKKQIE--- 56

QY 49 KSVLYFNRGISDIDLRLSKQAKYTVHFKNKTRKRVVDLKAGIHTADLINTSDIKAISVNV 108
Db 57 KNIFTNLNLNDILNSRLKRRKRYFL-----DVLESBLMQPKHISSNEYIIE 102

QY 109 TKKQVKDEKAKANVQPTITVNGTSQNT---LSNLTFFKKNQOISYKDLNNVSKVLKSN 165
Db 103 DSFKLLNSQKNTLLKSYKIKESVENDIKFAQEGISYKVKYKDLKSLKIKKVKIEE 162

QY 166 R-----GITDVLRLSKQAKFTVN---FKNGTKKV-----IDLKAGI 199
Db 163 KEKFPSSPPTTPPSAKTDEQKESKFLPFLNIETLYNNLVNKIDDDYLINLKAKI 218

RESULT 17
US-09-813-820-4
; Sequence 4, Application US/09813820
; Patent No. US20020102262A1
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; Patti, Joseph M.
; House-Pompeo, Karen
; Schanani, Narayana
; Symerky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433

; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,820
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/856,253
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-813-820-4

Query Match 11.2%; Score 114; DB 9; Length 211;
Best Local Similarity 23.9%; Pred. No. 0.32;
Matches 54; Conservative 28; Mismatches 84; Indels 60; Gaps 10;

QY 1 MRGSHHHHHCQSQPYTITVNGTSQNLSSLLTFNKNQOISYKDIENKVKSVLYFNRGISD 60
Db 1 MRGSHHHHHCQSQPYTITVNGTSQNLSSLLTFNKNQOISYKDIENKVKSVLYFNRGISD 60

QY 61 IDRLSKQAKYTVHFKNKTRKRVVDLKAGIHTADLINTS---DIKAISSNV----- 107
Db 47 -DM-LPETTHRVWFLNINNEKSYVSKDITTKDQIQGGQDLSTLINVTGTHSNYSG 104

QY 108 -----DTKKQVKDEKAKANVQPTITVNGTSQNLSSLLTFNKNQOISYKDIENKVKSVLYFN 148
Db 105 QSAITDFEKAFFGSKITVDNTKNTIDVTIPQGYSGSYNSFSINYKTKITNEQQKEFVNSQ 164

QY 149 ISYKD---LENNVKSV-----LKSNRGITDV---DLRLSKQAKFT 182
Db 165 AMYQEHGKEEVNGKSFNHTVHNINANAGIEGTGKGLKVLKQDKDT 210

RESULT 18
US-10-282-122A-53616
; Sequence 53616, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A

```
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53616
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53616

Query Match      11.2%; Score 113.5; DB 15; Length 246;
Best Local Similarity 22.0%; Pred. No. 0.43;
Matches 44; Conservative 40; Mismatches 65; Indels 51; Gaps 10;

QY 23 TSONILSSLTFFKNQOI---SYKDIEKVKSVLYFNRGISDIDLRLSKOAKYTVHFKNGT 79
Db 49 TKSNIWKELNVNLNENIPAYFKMKNK---LKNPYIENVEIKRPLNKKIISLKE-- 102
QY 80 KKV-----VDLKAGHTADLINTSIKA-----ISVNDTKQVKDKKAKANV 122
Db 103 KEIFAVLKDEDNYCYIDKKGNI--LEELRGSNESKDLIVDVSIDDKNSIKFRNKK--- 158
QY 123 QVPYTTITVNGTSONILSLTFFKNQO---QISYKDL--ENNKSVLKNRGTITVDLRLS 176
Db 159 -----TKENVFKTLNLYLKESGIYKPKINYVNLKESNIEMLTRSN-----IKILLS 203
QY 177 KOAKFTVNFKNGTKKVIDLK 196
Db 204 NDDNLDYNIISRVSKILIDLQ 223

RESULT 19
US-10-282-122A-61097
; Sequence 61097, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELI/RA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
```

```
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61097
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Legionella pneumophila
US-10-282-122A-61097

Query Match      10.9%; Score 111; DB 15; Length 963;
Best Local Similarity 21.6%; Pred. No. 3.7;
Matches 51; Conservative 46; Mismatches 73; Indels 66; Gaps 9;

QY 13 QIPYTTITV--GTSONILSSLTFFKNQOIYSYKDIENKVK----- 49
Db 119 KIELLTWNKKTIELIAETDLARQYQLLNDVNLKLVKXANFDLKEKLSIKAIRAKL 178
QY 50 ----SVLYFNRGISDID-----LRLSKOAKYTVHFKNGTKRVDLKAGIHTAD----- 93
Db 179 NKEINILYEN--AVSSQDKKQPELTISEQIOYEANLYINNQRIVAHQKLNALQLQKKI 237
QY 94 ----LINTSDIKAISVNDTKQVKDKREKANKANQVPTITVNGTSONILSLTFFKN--- 146
Db 238 TNLILLNLLDTKALQSADNRYREINQVS-----AIESLQTLISLTNQANLFPV 287
QY 147 ---QOISYKDLNNVSVLKNRGTITVDLRLSKOAKFTVNFKNGTKKVIDLKAGI 199
Db 288 EPGLQKSVSLQNDVKTTELKET---SNQKLILSKNLE---DYQNLQKKQISTROSL 337

RESULT 20
US-10-193-764-28
; Sequence 28, Application US/10193764
; Publication No. US20030133943A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
; FILE REFERENCE: 1038-1239MIS
; CURRENT APPLICATION NUMBER: US/10/193,764
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 09/167,568
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-28

Query Match      10.8%; Score 110; DB 14; Length 1220;
```



```
US-10-282-122A-70558
; Sequence 70558, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70558
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70558

Query Match      10.2%; Score 104; DB 15; Length 1051;
Best Local Similarity 25.9%; Pred. No. 15;
Matches 53; Conservative 29; Mismatches 69; Indels 54; Gaps 11;

QY 25 QNLSLTFNKNQOISYKDIENKVKSVLYFNRGISDIDLRLSKQAKYTVHFKNGT-----79
DB 50 QTTMSGATPQSTQDSISSKIDNQVSLAYVNSVQTE---SIPNASIVTVEYDNGTDMKA 106
QY 80 ----KRVVD---LKAGIHTADLINTS-----DIKAISSVNVDTKKQVKDKKAKANVQ-VPYT 127
DB 107 EQQLKKEIDKIKFKDGVGPELITRNSMDAPPVAVSFTSNNQK-LKDYTKLKNQQLVPKL 165
QY 128 ITVNTGTSQNLSNLTFFKNQOISYK-----DLNNVKSVL-----162
DB 166 QTIDGV-QN--AQLNGQTNREVSLFKQKNLDEKGLTANDVENYIKTATRETPPLGLGFQN 222
QY 163 KSNRGITVDLRLSKQAKFTVNFKN 187
DB 223 KSNKSIV-----VDGQFKSVDAFKN 242

RESULT 27
US-10-369-493-2021
; Sequence 2021, Application US/10369493

US-10-282-122A-60961
; Sequence 60961, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09

Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2021
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-2021

Query Match      10.2%; Score 103.5; DB 15; Length 609;
Best Local Similarity 24.9%; Pred. No. 8;
Matches 51; Conservative 29; Mismatches 56; Indels 69; Gaps 11;

QY 24 SQN--ILSSLTFNKNQOISYKDI--EN-KVKSVL-----YFNRGISDIDLRLSKQAKYT 72
DB 302 SQNDKILKLTNNKAYTKYKEVSLKKEAPKELDNESYNH-----DELLKKYKYT 356
QY 73 VHFKNGTKRVDLKGAIHTADLINTSDIKAISVNVDTKKQVKDKKAKAN-----121
DB 357 -----RETLDRVNRQQIILIDQNEFLKKSVMNQLQNEVNTATNFKSLFKE 400
QY 122 --VQVPTTYTNGTS-----QNLSNLTFFKNQO-----ISYKDLNNKSVLKSNGRITDV 171
DB 401 KYAKLADSITELNTSTKKEALGENLTTECHLEICLYK---KNENISNTNKNLQN- 456
QY 172 DLRLSKQAKFTVNFKNGTKKVIDLK 196
DB 457 -----SFKNERKKVLDLR 469

RESULT 28
US-10-282-122A-60961
; Sequence 60961, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
```

```
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60961
; LENGTH: 1778
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60961

Query Match          10.2%; Score 103.5; DB 15; Length 1778;
Best Local Similarity 20.2%; Pred. No. 31;
Matches 50; Conservative 38; Mismatches 73; Indels 87; Gaps 11;

Qy 17 TITVNGTSONILSLTFKNQOISYKDIENKVSPLYENRSGISDID-----62
Db 1014 TVTVNKDPAPISAKT-----EITDKSKKTEAAP-----LDDIDADTNDGSI VTSNFA 1063

Qy 63 --LRLSKQAKYTVHPKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQ-----112
Db 1064 TAVNLDKAGDVTVTLSINS---DGVAGTPTAIIVHVEKEKIATISTNTAQYKYAKIN 1120

Qy 113 ----VKKEKAN-----VQVP--YTIIVNGTSON-----136
Db 1121 ETQFLKDVHASINASPPTAVLESDETGVKLDVPGTYTITATNEDGGVAPKEVSIV 1180

Qy 137 -----ILSLFKKNQOISYKDLNNKVSULK--SNRGIT----DVDLRLSKQAKFTV 183
Db 1181 RKIPAPEITADKEIITPKFDEVSEAEFLNDIHATISDKNVAITSNFTSDVNLKAGDVTV 1240

Qy 184 NFKNGTKK 191
Db 1241 TL-NATNE 1247

RESULT 29
US-09-345-373-30
; Sequence 30, Application US/09345373
; Publication No. US20030077695A1
; GENERAL INFORMATION:
; APPLICANT: RUBEN, STEVEN M.
; APPLICANT: JIMENEZ, PABLO
; APPLICANT: DUAN, D. ROXANNE
; APPLICANT: RAMPY, MARK A.
; APPLICANT: MENDRICK, DONNA
; APPLICANT: ZHANG, JUN
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL A.
; APPLICANT: COLEMAN, TIMOTHY A.
; APPLICANT: GRUBER, JOACHIM R.
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: GENTZ, REINER L.
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: /09/345,373
; APPLICATION NUMBER: US/09/345,373
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,195
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,852
; FILING DATE: 13-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,045
; FILING DATE: 28-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,432
; FILING DATE: 23-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/910,875
; FILING DATE: 13-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/055,561
; FILING DATE: 13-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFEE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-345-373-30

Query Match          10.1%; Score 102.5; DB 10; Length 184;
Best Local Similarity 24.3%; Pred. No. 2.1;
Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

Qy 1 MRGSHHHHGSQIPYITVNGTSONILSLTFKNQOISYKDIENKVSPLYEN--RGI 58
Db 1 MRGSHHHHGS-----COALGQDMVSPPEATNSSSS--SFSPSSAGRHVRSYNHLOG- 51

Qy 59 SDIDLRLSKQAKYTVHF-----KN---GTRK-----VVDLKAGIHTADLINTSDIK 101
Db 52 ---DVRWRKLFSPFKYFKIEKNGKVGTKKENCPSYILEITSVEIGVAVKAINSYYL 108

Qy 102 AIS-----VNVDTKKQVKDKKAKANQVPPYITVNGTSONILSN 140
Db 109 AMNKKGLYSGKEFNNDCKLKERIEINGYNTYASFNMQHNGRQMYVALN 157

RESULT 30
US-10-075-446-30
; Sequence 30, Application US/10075446
; Publication No. US20030129687A1
; GENERAL INFORMATION:
; APPLICANT: RUBEN, STEVEN M.
; APPLICANT: JIMENEZ, PABLO
; APPLICANT: DUAN, D. ROXANNE
; APPLICANT: RAMPY, MARK A.
; APPLICANT: MENDRICK, DONNA
; APPLICANT: ZHANG, JUN
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL A.
; APPLICANT: COLEMAN, TIMOTHY A.
```



```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: POB60-Cys37 construct
US-10-901-210-30

Query Match      10.1%; Score 102.5; DB 17; Length 184;
Best Local Similarity 24.3%; Pred. No. 2.1;
Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

Qy 1 MRGSHHHHGGSGQIPYITVNGTSONILSLTFKKNQOISYKDIENKVKSVLYFN--RGI 58
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MRGSHHHHGGSG-----COALQDMVSPATNSSSS-SFSPSSAGRHVRSTNHLQG- 51

Qy 59 SDIDLRLSKQAKYTVHF-----KN-----GTRK-----VVDLKAGIHTADINTSDIK 101
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 52 ---DVRMRKLFSTFYFLKIEKNGKVGSTKKEKNCPSYLEITSVEIGVAVKAINSNYL 108
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

Qy 102 AIS-----VNVDTKKVKQDKEAKANVQVPYITVNGTSONILSN 140
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 109 AMNKKGLYGSKEFNNCKLRIEENGYNITYASFNQHNGRQMYVALN 157
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 33
US-10-404-667-2
; Sequence 2, Application US/10404667
; Publication No. US20040005332A1
; GENERAL INFORMATION:
; APPLICANT: Angov, Evelina
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Darko, Christian Asare
; APPLICANT: Cohen, Joe D.
; TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine
; CURRENT APPLICATION NUMBER: US/10/404,667
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 60/369,741
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/379,688
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Work XP
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P. falciparum (FVO) MSPI-42 (Mut 7, Pause Site mutant)
US-10-404-667-2

Query Match      10.0%; Score 101.5; DB 15; Length 371;
Best Local Similarity 22.7%; Pred. No. 6.2;
Matches 63; Conservative 34; Mismatches 80; Indels 101; Gaps 16;

Qy 4 SHHHHH--GSOIPYITVNGTSONILSLTFKKNQOISY-----KDIENKVK 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 AHHHHHPGGSGGTWAVTSPVIDNLSKI--ENEVEVLYLKLPLAGVYRSLKKQLEN--- 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 50 SVLYFNRGISDI-DLRLSKQ-----AKYTV-----HFKNGTKKVVDL 85
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 NVMTFNVNVKDIILNSRFNKNFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKDKFL 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 86 KAGIHTADLNT-----SDIKAISVNVDTKKQVKDKKEAKA----- 120
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 117 SSYNIKXSDTDINFANDVLGYGVKLSSEYKSKDLSI-----KYINDKQENEKYLFP 170
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

Qy 121 --NVQVPYITVNG-----TSQNTLSNLTFFKKNQOISYKDLNNKVS-----LKS 164
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 171 LNNIETLYK-TVNDKIDLFVHLEAEVLNVTYEKSNVEVKIKEL-NYLKTIQDKLADFKK 228
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

Qy 165 NR---GITDVL-----RLSKQAKFTVNFNGTKKVI 193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 229 NNNFVGIAIDLDYNNHNLITKFLSTGWFENPAKTVL 266
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 34
US-10-437-963-179404
; Sequence 179404, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 179404
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(775)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76870C.1.pap
US-10-437-963-179404

Query Match      10.0%; Score 101.5; DB 16; Length 775;
Best Local Similarity 24.7%; Pred. No. 16;
Matches 48; Conservative 34; Mismatches 75; Indels 37; Gaps 9;

Qy 21 NGTSONILSLTFKKNQOISYKDIENKVKSVLYFNKQISIDILR-----LSKQAKYTV--- 73
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 494 NTSKKSIIINSSENSNVQPNNTASVGNR-----NSKIDVNSNTGSIITKDSKNTVWKP 546
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

Qy 74 ---HFKNGTKKRVVDLKAGIHTADLINTSDIKAISVNVDTKK---QVKDKKAKANVQVPYT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 SIGSFVNRNATVDVKPNI--GSITSRGDS--DTKSNIGSVASKDAKTIDAKEPST 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 128 ITVNGTSONI---LSNLTFFKKNQOISYKDLNNKVSVLKSNRGITDVLRLSKQAKFTVN 184
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 600 SSITSQDSKIGDGRSNDIGIANRDAKTADVKNIRSVV--NTYLRNFDVKHN-----TGN 652
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

Qy 185 FKNGTKKVIDLKAG 198
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 653 IVDGGVKHSDLKPG 666
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 35
US-09-841-786-1
; Sequence 1, Application US/09841786
; Patent No. US20020054883A1
; GENERAL INFORMATION:
; APPLICANT: NAGARAJA, T. G.
; APPLICANT: STEWART, GEORGE C.
; APPLICANT: NARAYANAN, SANJEEV K.
; APPLICANT: CHENGAPPA, M. M.
; TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
; FILE REFERENCE: 30296
; CURRENT APPLICATION NUMBER: US/09/841,786
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/558,257
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

```

[illegible]

```
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNKGTKRVDLKGAIHTADLIN-TS 98
DB 918 GGLFDNKGNSISIAKGGARFKDIDNSKNLSITNSSSTYRTII-----SGNITNKNG 970
QY 99 DIKAISVNVDTKKQ---VKDKEAKANVQVPYITVNGTSQNILSLTFKK--NQOISYK 152
DB 971 DLNITNEGSDTEMQIGGDSVQKEG-----NLTISDKINITYKQITIKAGVDGENSDS 1022
QY 153 DLENNVKSVLKSNRGITDVLRLSKQAKFTVNFKNKGTKKVIDLKAG 198
DB 1023 DATNNANLTIKTKEKLKLTQDLNLSGNFKAEITAKDGS----DLTIG 1064
```

```
RESULT 39
US-10-193-764-63
; Sequence 63, Application US/10193764
; Publication No. US20030133943A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
; TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
; FILE REFERENCE: 1038-1239MIS
; CURRENT APPLICATION NUMBER: US/10/193,764
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 09/167,568
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1536
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-63
```

```
Query Match 9.9%; Score 101; DB 14; Length 1536;
Best Local Similarity 23.9%; Pred. No. 40;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

QY 3 GSHHHHHHGSQIPYTI-----TVNGTSQNILSLTFKNKQOISYKDIENTKSV 51
DB 863 GSDFDNH---OKPLTIKKDVIINSGLTAGGNIVNIAGNLTVESN--ANFKAITNFTFNV 917
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNKGTKRVDLKGAIHTADLIN-TS 98
DB 918 GGLFDNKGNSISIAKGGARFKDIDNSKNLSITNSSSTYRTII-----SGNITNKNG 970
QY 99 DIKAISVNVDTKKQ---VKDKEAKANVQVPYITVNGTSQNILSLTFKK--NQOISYK 152
DB 971 DLNITNEGSDTEMQIGGDSVQKEG-----NLTISDKINITYKQITIKAGVDGENSDS 1022
QY 153 DLENNVKSVLKSNRGITDVLRLSKQAKFTVNFKNKGTKKVIDLKAG 198
DB 1023 DATNNANLTIKTKEKLKLTQDLNLSGNFKAEITAKDGS----DLTIG 1064
```

```
RESULT 40
US-10-681-171-2
; Sequence 2, Application US/10681171
; Publication No. US20050053618A1
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen J.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS OF NON-TYPEABLE
; FILE REFERENCE: 5346
; CURRENT APPLICATION NUMBER: US/10/681,171
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: 09/155,614
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/617,697
; PRIOR FILING DATE: 1996-04-01
```

```
; PRIOR APPLICATION NUMBER: PCT/US97/04707
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1536
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-681-171-2
```

```
Query Match 9.9%; Score 101; DB 17; Length 1536;
Best Local Similarity 23.9%; Pred. No. 40;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

QY 3 GSHHHHHHGSQIPYTI-----TVNGTSQNILSLTFKNKQOISYKDIENTKSV 51
DB 863 GSDFDNH---OKPLTIKKDVIINSGLTAGGNIVNIAGNLTVESN--ANFKAITNFTFNV 917
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNKGTKRVDLKGAIHTADLIN-TS 98
DB 918 GGLFDNKGNSISIAKGGARFKDIDNSKNLSITNSSSTYRTII-----SGNITNKNG 970
QY 99 DIKAISVNVDTKKQ---VKDKEAKANVQVPYITVNGTSQNILSLTFKK--NQOISYK 152
DB 971 DLNITNEGSDTEMQIGGDSVQKEG-----NLTISDKINITYKQITIKAGVDGENSDS 1022
QY 153 DLENNVKSVLKSNRGITDVLRLSKQAKFTVNFKNKGTKKVIDLKAG 198
DB 1023 DATNNANLTIKTKEKLKLTQDLNLSGNFKAEITAKDGS----DLTIG 1064
```

Search completed: March 16, 2005, 10:55:25
Job time : 139 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 10:36:37 ; Search time 43 Seconds
(without alignments)
347.205 Million cell updates/sec

Title: US-10-041-775-2
Perfect score: 1016
Sequence: 1 MRGSHHHHGSQIPYITTV.....FTVFNKGTGKVIDLKAGIY 200

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	950	93.5	689	1	US-08-248-021A-2
2	440	43.3	150	4	US-08-956-171E-5238
3	440	43.3	150	4	US-08-781-986A-5238
4	210	20.7	151	4	US-08-956-171E-5233
5	210	20.7	151	4	US-08-781-986A-5233
6	159	15.6	31	1	US-08-248-021A-3
7	155	15.3	31	1	US-08-248-021A-4
8	116.5	11.5	512	3	US-08-856-253-6
9	114	11.2	211	3	US-08-856-253-4
10	110	10.8	31	1	US-08-248-021A-7
11	110	10.8	1095	4	US-09-206-942-45
12	110	10.8	1101	4	US-09-206-942-43
13	110	10.8	1220	4	US-09-206-942-28
14	110	10.8	1226	4	US-09-206-942-25
15	108.5	10.7	288	3	US-09-134-001C-4005
16	106	10.4	345	3	US-08-856-253-7
17	104	10.2	74	4	US-09-490-291-11
18	104	10.2	159	3	US-08-856-253-2
19	104	10.2	1051	3	US-09-134-001C-5005
20	103.5	10.2	609	4	US-09-538-092-711
21	102.5	10.1	184	3	US-09-023-082A-30
22	102.5	10.1	184	4	US-09-248-998-30
23	102.5	10.1	184	4	US-09-610-651-30
24	101.5	10.0	3241	4	US-09-841-786-1
25	101	9.9	1095	4	US-09-206-942-69
26	101	9.9	1536	1	US-08-038-682-2
27	101	9.9	1536	1	US-08-302-832-2

28	101	9.9	1536	2	US-08-530-198-2	Sequence 2, Appli
29	101	9.9	1536	2	US-08-469-880-2	Sequence 2, Appli
30	101	9.9	1536	2	US-08-728-470-2	Sequence 2, Appli
31	101	9.9	1536	2	US-08-617-697-2	Sequence 2, Appli
32	101	9.9	1536	3	US-08-719-641-2	Sequence 2, Appli
33	101	9.9	1536	4	US-09-206-942-67	Sequence 67, Appli
34	99.5	9.8	1207	4	US-09-978-594-4	Sequence 4, Appli
35	97.5	9.6	297	4	US-10-030-031A-2	Sequence 2, Appli
36	97.5	9.6	333	4	US-09-248-796A-15901	Sequence 15901, A
37	96.5	9.5	789	4	US-09-604-958-1	Sequence 1, Appli
38	96.5	9.5	789	4	US-09-995-587A-1	Sequence 1, Appli
39	95.5	9.4	221	1	US-08-621-081A-19	Sequence 19, Appli
40	95	9.4	331	4	US-09-107-433-3308	Sequence 3308, Ap
41	95	9.4	447	3	US-08-961-083-182	Sequence 182, App
42	95	9.4	447	4	US-09-536-784-182	Sequence 182, App
43	95	9.4	484	4	US-09-468-656A-6	Sequence 6, Appli
44	95	9.4	1039	4	US-09-583-110-5226	Sequence 5226, Ap
45	94.5	9.3	1231	4	US-09-071-035-420	Sequence 420, App

ALIGNMENTS

RESULT 1
US-08-248-021A-2
; Sequence 2, Application US/08248021A
; Patent No. 5648240
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Jonsson, Klas
; APPLICANT: Patti, Joseph M.
; APPLICANT: Gurusiddappa, Sivashankarappa
; TITLE OF INVENTION: MHC II ANALOG FROM STAPHYLOCOCCUS AUREUS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,021A
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TANK:155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 689 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-248-021A-2

Query Match 93.5%; Score 950; DB 1; Length 689;
Best Local Similarity 97.0%; Pred. No. 7.5e-82;
Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 4 SHHHHGSQIPYITTVNGTSQNTLSSTFNKNQOISYKDIENKVKSVLYFNRGISDIDL 63
DB 41 SLHHGYSKIQIPYITTVNGTSQNTLSSTFNKNQOISYKDIENKVKSVLYFNRGISDIDL 100

Qy 64 RLSKQAKYTVHFKNQTKRVVDLKGAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ 123
Db 101 RLSKQAKYTVHFKNQTKRVVDLKGAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ 160
Qy 124 VPYITVNGTSONILSNLTFKKNQOISYKDLNNVKSVLKSNRGIITVDLRLSKQAKFTV 183
Db 161 VPYITVNGTSONILSNLTFKKNQOISYKDLNNVKSVLKSNRGIITVDLRLSKQAKFTV 220
Qy 184 NFKNGTKKVIDLKAGIY 200
Db 221 NFKNGTKKVIDLKAGIY 237

RESULT 2
US-08-956-171E-5238
; Sequence 5238, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5238:
US-08-956-171E-5238

Query Match 43.3%; Score 440; DB 4; Length 150;
Best Local Similarity 78.9%; Pred. No. 2.6e-34;
Matches 86; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 4 SHHHHHGSGIPYITVNGTSONILSNLTFKKNQOISYKDLNNVKSVLKSNRGIITVDLRLSKQAKFTV 63
Db 42 SLHHGYSKVHVPYAITVNGTSONILSNLTFKKNQOISYKDLNNVKSVLKSNRGIITVDLRLSKQAKFTV 101
Qy 64 RLSKQAKYTVHFKNQTKRVVDLKGAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ 112
Db 102 RLSKQAKYTVHFKNQTKRVVDLKGAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ 150

RESULT 4
US-08-956-171E-5233
; Sequence 5233, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256

Db 102 RLSKQAKYTVHFKNQTKRVVDLKGAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ 150

RESULT 3
US-08-781-986A-5238
; Sequence 5238, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-986A-5238

Query Match 43.3%; Score 440; DB 4; Length 150;
Best Local Similarity 78.9%; Pred. No. 2.6e-34;
Matches 86; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 4 SHHHHHGSGIPYITVNGTSONILSNLTFKKNQOISYKDLNNVKSVLKSNRGIITVDLRLSKQAKFTV 63
Db 42 SLHHGYSKVHVPYAITVNGTSONILSNLTFKKNQOISYKDLNNVKSVLKSNRGIITVDLRLSKQAKFTV 101
Qy 64 RLSKQAKYTVHFKNQTKRVVDLKGAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ 112
Db 102 RLSKQAKYTVHFKNQTKRVVDLKGAGIHTADLINTSDIKAISVNVDTTKQVKDKKAKANVQ 150

RESULT 4
US-08-956-171E-5233
; Sequence 5233, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256


```

; TOPOLOGY: linear
US-08-248-021A-3

Query Match          15.6%; Score 159; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 DIDRLRSKQAKYTVHFKNGTKRVVLDLKAGIH 90
Db 1 DIDRLRSKQAKYTVHFKNGTKRVVLDLKAGIH 31

RESULT 7
US-08-248-021A-4
; Sequence 4, Application US/08248021A
; Patent No. 5648240
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Jonsson, Klas
; APPLICANT: Patti, Joseph M.
; APPLICANT: Gurusiddappa, Sivashankarappa
; TITLE OF INVENTION: MHC II ANALOG FROM STAPHYLOCOCCUS AUREUS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/248,021A
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-248-021A-4

Query Match          15.3%; Score 155; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 DVDRLRSKQAKFTVHFKNGTKRVVLDLKAGIY 200
Db 1 DVDRLRSKQAKFTVHFKNGTKRVVLDLKAGIY 31

RESULT 8
US-08-856-253-6
; Sequence 6, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS

; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/856,253
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,678
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TAMK:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-856-253-6

Query Match          11.5%; Score 116.5; DB 3; Length 512;
Best Local Similarity 23.8%; Pred. No. 0.0085;
Matches 64; Conservative 29; Mismatches 79; Indels 97; Gaps 14;

QY 1 MRGSHHHHGGSQIPYITVNGTSQNILSS-----LTF-NKQOISYKD----- 43
Db 1 MRGSHHHHGGARDISST-NVTLTVSPSKIEDGGKTTVMKTPDDKNGKIQNGDMIKVA 59
QY 44 -----IENKVKSV-----LYEN-----RGISDIDLRLSKQAKYT 72
Db 60 WPTSGTVKIEGYKTVPLTVKGEQVQAVTPDGAITTFNDKVKLSDV-----SGFAEFE 115
QY 73 VHFKNKGRVVDLKGAIHTADLINTSDIKAISV---NVDTKKQVKQKEA----- 118
Db 116 VQGNLTQ-----TNTSDDKVAITISGNKSTNVTVKSEAGTSSVFFYKGT 161
QY 119 ----KANVQVPYITVNGTSQNILSNLTFKK-----NQOISYKDLNNV-----KSVLKSNR 166
Db 162 DMLPEDTTHVRWFLNNINKEYSVSKDITIKDIQIQGGQQLDLSTLNINVTGTHSNYSYQS 221
QY 167 GITDVDLRLSKQAKFTVHFKNGTKRVVLDL 195
Db 222 AITDFE-KAPFGSKITV---DNTKNTIDV 246

RESULT 9
US-08-856-253-4
; Sequence 4, Application US/08856253
; Patent No. 6288214
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Patti, Joseph M.
; APPLICANT: House-Pompeo, Karen
; APPLICANT: Sthanam, Narayana
; APPLICANT: Symersky, Jindrich
; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS

```


QY 175 LSKQAKFTVNFNGTKKVI 193
Db 605 ISGFDKAEITAKEGADLII 623

RESULT 12
US-09-206-942-43
; Sequence 43, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; TITLE OF INVENTION: Molecular Weight Proteins
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 1101
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-43

Query Match 10.8%; Score 110; DB 4; Length 1101;
Best Local Similarity 25.1%; Pred. No. 0.11;
Matches 50; Conservative 29; Mismatches 76; Indels 44; Gaps 8;

QY 18 ITVNGTSQNLSSLT-----FNKQOISYKDIENKVKSVLYFNRCISDIDLRLSKQAKY 71
Db 452 LTVTGSAINLEKNLTVEGSAFLANPNYSFN-----VSLFDNQKGSNISI-----AKG 500
QY 72 TVHFK--NGTKRVVDLKAGIHTADLINTSD-----IKAISVNVDTKKQVKDKKAKANVQ 123
Db 501 GAHFKDINNTK-----SLNITNDSAVRTIIEGNIITNSGDLNITDNKNNAEIQ 550
QY 124 VPTYI-----TVNGTSQNLSSLTFFK--NQOISYKDLNENKVKSVLKNRGITDVLRL 174
Db 551 ICGNISQKGNLTISDDKINITNQITIKGVNKKEDSDSDSTANNANLTIKTELQLTGDLN 610
QY 175 LSKQAKFTVNFNGTKKVI 193
Db 611 ISGFDKAEITAKEGADLII 629

RESULT 13
US-09-206-942-28
; Sequence 28, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; TITLE OF INVENTION: Molecular Weight Proteins
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-28

Query Match 10.8%; Score 110; DB 4; Length 1220;
Best Local Similarity 23.7%; Pred. No. 0.12;
Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;

QY 3 GSHHHHHGSGIPTYI-----TVNGTSQNLSSLTFFNKNQOISYKDIENKVKSV 51
Db 422 GSDFDNH---QKPLTIKKDVIINSNLTAGGNVINGNLTVNNGANL--KAITNFTFNV 476
QY 52 --LYFNRCISDIDLRLSKQAKYTVHFKNGTFRVVDLKAGIHTADLINTSDIKAISVNVDT 109
Db 477 GGLFDNKGNSNISI-----ARGGAKFKDINNTSSLN-ITNDS 514
QY 110 KKQ-----VKDKKAKANVQVPYTI-----TVNGTSQNLSSLTFFK-- 145
Db 515 TYRTIIEGNIITNKGADLNIIDNKGNAEIQIGGNISQKGNLTISDDKINITNQITIKGV 574
QY 146 NQOISYKDLNENKVKSVLKNRGITDVLRLSKQAKFTVNFNKGTKKVI 193
Db 575 NKEDSDSDSTANNANLTIKTELQLTGDLNISGFDKAEITAKEGADLII 622

RESULT 14
US-09-206-942-26
; Sequence 26, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; TITLE OF INVENTION: Molecular Weight Proteins
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1226
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-26

Query Match 10.8%; Score 110; DB 4; Length 1226;
Best Local Similarity 23.7%; Pred. No. 0.12;
Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;

QY 3 GSHHHHHGSGIPTYI-----TVNGTSQNLSSLTFFNKNQOISYKDIENKVKSV 51
Db 428 GSDFDNH---QKPLTIKKDVIINSNLTAGGNVINGNLTVNNGANL--KAITNFTFNV 482
QY 52 --LYFNRCISDIDLRLSKQAKYTVHFKNGTFRVVDLKAGIHTADLINTSDIKAISVNVDT 109
Db 483 GGLFDNKGNSNISI-----ARGGAKFKDINNTSSLN-ITNDS 520
QY 110 KKQ-----VKDKKAKANVQVPYTI-----TVNGTSQNLSSLTFFK-- 145
Db 521 TYRTIIEGNIITNKGADLNIIDNKGNAEIQIGGNISQKGNLTISDDKINITNQITIKGV 580
QY 146 NQOISYKDLNENKVKSVLKNRGITDVLRLSKQAKFTVNFNKGTKKVI 193
Db 581 NKEDSDSDSTANNANLTIKTELQLTGDLNISGFDKAEITAKEGADLII 628

RESULT 15
US-09-134-001C-4005
; Sequence 4005, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

Db 457 -----SPKNERKKVLDLR 469

RESULT 21

US-09-023-082A-30

Sequence 30, Application US/09023082A

Patent No. 6077692

GENERAL INFORMATION:

APPLICANT: RUBEN, STEVEN M.

APPLICANT: JIMENEZ, PABLO

APPLICANT: DUAN, D. ROXANNE

APPLICANT: RAMPY, MARK A.

APPLICANT: MENDRICK, DONNA

APPLICANT: ZHANG, JUN

APPLICANT: NI, JIAN

APPLICANT: MOORE, PAUL A.

APPLICANT: COLEMAN, TIMOTHY A.

APPLICANT: GRUBER, JOACHIM R.

APPLICANT: DILLON, PATRICK J.

APPLICANT: GENTZ, REINER L.

TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 NEW YORK AVE, NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,082A

FILING DATE: 13-FEB-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01790

FILING DATE: 14-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/461,195

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/023,852

FILING DATE: 13-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/039,045

FILING DATE: 28-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/862,432

FILING DATE: 23-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/910,875

FILING DATE: 13-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/055,561

FILING DATE: 13-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0360008/EKS

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-023-082A-30

Query Match 10.1%; Score 102.5; DB 3; Length 184;

Best Local Similarity 24.3%; Pred. No. 0.043;

Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

QY 1 MRGSHHHHGSQIPYITVNGTSQNILSSLTFFKNQOISYKDINKVKSVLYFN--RGI 58

Db 1 MRGSHHHHHS-----COALGDMVSPPEATNSSSS-SFSSPSSAGRHVRSYNHLQ- 51

QY 59 SDIDLRLSKQAKYTVHF-----KN-----GTRK-----VVDLKAGIHTADLINTSDIK 101

Db 52 ---DVRWKLFSPFKYFKIEKNGKVGSTKKEKPCYSILEITSVEIGVAVKAINSYL 108

QY 102 AIS-----VNVDTKKQVKDEAKANQVQPYITVNGTSQNILSN 140

Db 109 AMNKKGLYGSKEFNNDCKLKERIEENGYNITYASFNMQHNGRMVVALN 157

RESULT 22

US-09-248-998-30

Sequence 30, Application US/09248998

Patent No. 6599879

GENERAL INFORMATION:

APPLICANT: Jimenez, Pablo

APPLICANT: Rampy, Mark A.

APPLICANT: Mendrick, Donna

APPLICANT: Russell, Deborah

APPLICANT: Louie, Arthur

TITLE OF INVENTION: Therapeutic Uses of Keratinocyte Growth Factor-2

FILE REFERENCE: 1488.1060002

CURRENT APPLICATION NUMBER: US/09/248,998

CURRENT FILING DATE: 1999-02-12

EARLIER APPLICATION NUMBER: US 60/114,387

EARLIER FILING DATE: 30-DEC-1998

EARLIER APPLICATION NUMBER: US 60/074,585

EARLIER FILING DATE: 13-FEB-1998

NUMBER OF SEQ ID NOS: 148

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 30

LENGTH: 184

TYPE: PRT

ORGANISM: Homo sapiens

US-09-248-998-30

Query Match 10.1%; Score 102.5; DB 4; Length 184;

Best Local Similarity 24.3%; Pred. No. 0.043;

Matches 41; Conservative 26; Mismatches 61; Indels 41; Gaps 8;

QY 1 MRGSHHHHGSQIPYITVNGTSQNILSSLTFFKNQOISYKDINKVKSVLYFN--RGI 58

Db 1 MRGSHHHHHS-----COALGDMVSPPEATNSSSS-SFSSPSSAGRHVRSYNHLQ- 51

QY 59 SDIDLRLSKQAKYTVHF-----KN-----GTRK-----VVDLKAGIHTADLINTSDIK 101

Db 52 ---DVRWKLFSPFKYFKIEKNGKVGSTKKEKPCYSILEITSVEIGVAVKAINSYL 108

QY 102 AIS-----VNVDTKKQVKDEAKANQVQPYITVNGTSQNILSN 140

Db 109 AMNKKGLYGSKEFNNDCKLKERIEENGYNITYASFNMQHNGRMVVALN 157

RESULT 23

US-09-610-651-30

Sequence 30, Application US/09610651

Patent No. 6693077

GENERAL INFORMATION:

APPLICANT: Ruben, Steven M.

APPLICANT: Jimenez, Pablo

APPLICANT: Duan, D. Roxanne

APPLICANT: Rampy, Mark A.

APPLICANT: Mendrick, Donna

APPLICANT: Zhang, Jun

APPLICANT: Ni, Jian

QY 3 GSHHHHGSQIPYTI-----TVNGTSQNLSSLTFNKNQOISYKDIENKVKSV 51
DB 422 GSDFDNH---QRPLTIKDVIIINSGLNTAGGIVNIAGNLTVESN--ANFKAITNFTFNV 476
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNGTKRVDLKGAGIHTADLIN-TS 98
DB 477 GGLFDNKGNSNLSIAKGARFKDIDNSKLSITTNSSSTYRTII-----SGNITNKG 529
QY 99 DIKAIISVNVDTKKQ-----VKDKEAKANVQVPYITVNGTSQNLSSLNLTFFKK--NQOISYK 152
DB 530 DLNITNEGSDTEMQIGDVSQKEG-----NLTISSDKINITKQITIKAGVDGENSDS 581
QY 153 DLENNVKSVLKNSRGITVDLRLSKQAKFTVNFKNGTKKVIDLKAG 198
DB 582 DATNANLTIKTKEKLTQDLNLSGFKAEITAKDGS-----DLTIG 623

RESULT 26

US-08-038-682-2
; Sequence 2, Application US/08038682
; Patent No. 5549897
; GENERAL INFORMATION:
; APPLICANT: BARENKAMP, STEPHEN J
; APPLICANT: ST. GEORGE III, JOSEPH W
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
; TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,682
; FILING DATE: 16-MAR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BERKSTRESSER, JERRY W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1536 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-038-682-2

Query Match 9.9%; Score 101; DB 1; Length 1536;
Best Local Similarity 23.9%; Pred. No. 1.2;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

QY 3 GSHHHHGSQIPYTI-----TVNGTSQNLSSLTFNKNQOISYKDIENKVKSV 51
DB 863 GSDFDNH---QRPLTIKDVIIINSGLNTAGGIVNIAGNLTVESN--ANFKAITNFTFNV 917
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNGTKRVDLKGAGIHTADLIN-TS 98
DB 918 GGLFDNKGNSNLSIAKGARFKDIDNSKLSITTNSSSTYRTII-----SGNITNKG 970
QY 99 DIKAIISVNVDTKKQ-----VKDKEAKANVQVPYITVNGTSQNLSSLNLTFFKK--NQOISYK 152

DB 971 DLNITNEGSDTEMQIGDVSQKEG-----NLTISSDKINITKQITIKAGVDGENSDS 1022
QY 153 DLENNVKSVLKNSRGITVDLRLSKQAKFTVNFKNGTKKVIDLKAG 198
DB 1023 DATNANLTIKTKEKLTQDLNLSGFKAEITAKDGS-----DLTIG 1064

RESULT 27

US-08-302-832-2
; Sequence 2, Application US/08302832
; Patent No. 5603938
; GENERAL INFORMATION:
; APPLICANT: BARENKAMP, STEPHEN J
; TITLE OF INVENTION: High Molecular Weight Surface Proteins
; TITLE OF INVENTION: of No. 5603938-Typeable Haemophilus
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd.
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,832
; FILING DATE: 16-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9205704.1
; FILING DATE: 16-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US pct/us93/02166
; FILING DATE: 16-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Berkstresser, Jerry W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-404
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1536 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-302-832-2

Query Match 9.9%; Score 101; DB 1; Length 1536;
Best Local Similarity 23.9%; Pred. No. 1.2;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

QY 3 GSHHHHGSQIPYTI-----TVNGTSQNLSSLTFNKNQOISYKDIENKVKSV 51
DB 863 GSDFDNH---QRPLTIKDVIIINSGLNTAGGIVNIAGNLTVESN--ANFKAITNFTFNV 917
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNGTKRVDLKGAGIHTADLIN-TS 98
DB 918 GGLFDNKGNSNLSIAKGARFKDIDNSKLSITTNSSSTYRTII-----SGNITNKG 970
QY 99 DIKAIISVNVDTKKQ-----VKDKEAKANVQVPYITVNGTSQNLSSLNLTFFKK--NQOISYK 152
DB 971 DLNITNEGSDTEMQIGDVSQKEG-----NLTISSDKINITKQITIKAGVDGENSDS 1022
QY 153 DLENNVKSVLKNSRGITVDLRLSKQAKFTVNFKNGTKKVIDLKAG 198

Db 1023 DATNNANLTKTKELKLTQDLNLSGFNKAETAKDGS-----DLTIG 1064

RESULT 28

US-08-530-198-2
; Sequence 2, Application US/08530198

; Patent No. 5869065
; GENERAL INFORMATION:

; APPLICANT: BARENKAMP, STEPHEN J
; APPLICANT: ST. GENE III, JOSEPH W
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
; TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; STREET: Bldg. 1
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,198
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: BERKSTRESSER, JERRY W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: JWB-1186
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1536 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-530-198-2

Query Match 9.9%; Score 101; DB 2; Length 1536;
Best Local Similarity 23.9%; Pred. No. 1.2;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

QY 3 GSHHHHHGSGIPIYTI-----TVNGTSQNLSSLTFNKQIQISYKDIENKVKSV 51
Db 863 GSDFDNH---QKPLTIKKDVIINSGLTAGNIVNIAGNLTVESN--ANFKAITFTFNV 917

QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNGTGRVVDLKGAIHTADLIN-TS 98
Db 918 GGLFDNKGNSISIAKGGARFKDIDNSKLSITNSSSTYRTII-----SGNITNKG 970

QY 99 DIKAISVNDTKQ-----VKDKEAKANVQVPYITVNGTSQNLNLTFFKK--NQOISYK 152
Db 971 DLNITNEGSDTEMIIGDVSQKEG-----NLTISSDKINITKQITIKAGVDGENSDS 1022

QY 153 DLENNVKSVLKNSRGITDVLRLSKQAKFTVNFKNGTKKVIDLKAG 198
Db 1023 DATNNANLTKTKELKLTQDLNLSGFNKAETAKDGS-----DLTIG 1064

RESULT 29

US-08-469-880-2

; Sequence 2, Application US/08469880
; Patent No. 5876733

; GENERAL INFORMATION:

; APPLICANT: Barenkamp, Stephen J.
; TITLE OF INVENTION: High Molecular Weight Surface Proteins
; TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Shoemaker and Mattare, Ltd.
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; STREET: Bldg. 1
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,880
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9205704.1
; FILING DATE: 16-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/02166
; FILING DATE: 16-MAR-1993

; APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,832
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: Berkstresser, Jerry W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-516 MIS-VG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1536 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-469-880-2

Query Match 9.9%; Score 101; DB 2; Length 1536;
Best Local Similarity 23.9%; Pred. No. 1.2;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;

QY 3 GSHHHHHGSGIPIYTI-----TVNGTSQNLSSLTFNKQIQISYKDIENKVKSV 51
Db 863 GSDFDNH---QKPLTIKKDVIINSGLTAGNIVNIAGNLTVESN--ANFKAITFTFNV 917

QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNGTGRVVDLKGAIHTADLIN-TS 98
Db 918 GGLFDNKGNSISIAKGGARFKDIDNSKLSITNSSSTYRTII-----SGNITNKG 970

QY 99 DIKAISVNDTKQ-----VKDKEAKANVQVPYITVNGTSQNLNLTFFKK--NQOISYK 152
Db 971 DLNITNEGSDTEMIIGDVSQKEG-----NLTISSDKINITKQITIKAGVDGENSDS 1022

QY 153 DLENNVKSVLKNSRGITDVLRLSKQAKFTVNFKNGTKKVIDLKAG 198
Db 1023 DATNNANLTKTKELKLTQDLNLSGFNKAETAKDGS-----DLTIG 1064

RESULT 30

US-08-728-470-2

; Sequence 2, Application US/08728470
; Patent No. 5928651

; GENERAL INFORMATION:

; APPLICANT: Barenkamp, Stephen J

;; TITLE OF INVENTION: High Molecular Weight Surface Proteins
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Shoemaker and Mattare, Ltd.
;; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202-0286
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/728,470
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/302,832
;; FILING DATE: 16-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US PCT/US93/02166
;; FILING DATE: 16-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9205704.1
;; FILING DATE: 16-MAR-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Berkstresser, Jerry W
;; REGISTRATION NUMBER: 22,651
;; REFERENCE/DOCKET NUMBER: 1038-633
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 415-0810
;; TELEFAX: (703) 415-0813
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1536 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE:
US-08-728-470-2

Query Match 9.9%; Score 101; DB 2; Length 1536;
Best Local Similarity 23.9%; Pred. No. 1.2;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;
QY 3 GSHHHHGGSQIPYTI-----TVNGTSQNILSLTFNKNQOISYKDIENKVKSV 51
DB 863 GSDFDNH---QKPLTIKKDVIINSGLTAGNIVNIAGNLTVESN--ANFKAITNFTFNV 917
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNKGTKRVDLKGAIHTADLIN-TS 98
DB 918 GGLFNDKGNISIAKGGARFKDIDNSKNLSITTSNSTYRTII-----SGNITKNG 970
QY 99 DIKAIENVVDTKQ-----VKDKEAKANVQVPTITVNGTSQNILSLTFKK--NQOISYK 152
DB 971 DLNITNEGSDTEWQIGDVSQKEG-----NLTISSDKINITKQITIKAGVDGENSDS 1022
QY 153 DLNNVKSVLKSNRGITDVLRLSKQAKFTVNFKNKGTKKVIDLKAG 198
DB 1023 DATNNANLTIKTKEKLQDLNLSGPNKAEITAKDGS-----DLTIG 1064

RESULT 31
US-08-617-697-2
; Sequence 2, Application US/08617697
; Patent No. 5977336
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen J
; TITLE OF INVENTION: High Molecular Weight Surface Proteins

;; TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Shoemaker and Mattare, Ltd.
;; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22202-0286
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/617,697
;; FILING DATE: 01-APR-1996
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/302,832
;; FILING DATE: 05-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US PCT/US93/02166
;; FILING DATE: 16-MAR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Berkstresser, Jerry W
;; REGISTRATION NUMBER: 22,651
;; REFERENCE/DOCKET NUMBER: 1038-557
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 415-0810
;; TELEFAX: (703) 415-0813
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1536 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-617-697-2

Query Match 9.9%; Score 101; DB 2; Length 1536;
Best Local Similarity 23.9%; Pred. No. 1.2;
Matches 54; Conservative 32; Mismatches 86; Indels 54; Gaps 11;
QY 3 GSHHHHGGSQIPYTI-----TVNGTSQNILSLTFNKNQOISYKDIENKVKSV 51
DB 863 GSDFDNH---QKPLTIKKDVIINSGLTAGNIVNIAGNLTVESN--ANFKAITNFTFNV 917
QY 52 --LYFNRGISDI-----DLRLSKQAKYTVHFKNKGTKRVDLKGAIHTADLIN-TS 98
DB 918 GGLFNDKGNISIAKGGARFKDIDNSKNLSITTSNSTYRTII-----SGNITKNG 970
QY 99 DIKAIENVVDTKQ-----VKDKEAKANVQVPTITVNGTSQNILSLTFKK--NQOISYK 152
DB 971 DLNITNEGSDTEWQIGDVSQKEG-----NLTISSDKINITKQITIKAGVDGENSDS 1022
QY 153 DLNNVKSVLKSNRGITDVLRLSKQAKFTVNFKNKGTKKVIDLKAG 198
DB 1023 DATNNANLTIKTKEKLQDLNLSGPNKAEITAKDGS-----DLTIG 1064

RESULT 32
US-08-719-641-2
; Sequence 2, Application US/08719641
; Patent No. 6218141
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen J
; TITLE OF INVENTION: High Molecular Weight Surface Proteins
; TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd.

US-09-995-587A-1

Query Match 9.5%; Score 96.5; DB 4; Length 789;
Best Local Similarity 24.9%; Pred. No. 1.3;
Matches 48; Conservative 31; Mismatches 87; Indels 27; Gaps 8;

QY 19 TVNGTSONILSFLFNKNQIISYKDIENKVKSVLYFNRI---SDIDLRLS---KQKYYT 72
DB 24 TVNASADTNIEN-NDSSVTQVTTGNDIAVKSVTILGSGQVSAASDITRTSANANSASSA 82

QY 73 VHFKNKTKRVVD---LKAGIHTADLINTSDIKALSIVNVD--KKQVKDEAKAN---VQV 124
DB 83 ANTONSNSQVASSAAITSTSSAASLNNTDSKAAQENTNTAKNDTQKAPANESSAKN 142

QY 125 PYTIVNGTS-----QNILSNITFFKNQIQISYKDIENNVKSVLKNRGITVDVLRSLK 177
DB 143 EPAVNVNDSSAAKNDQSSKNTAKLN-----KDAENVVKAGIDPNSLTDDQIKALN 197

QY 178 QAKFTVNFKNKTK 190
DB 198 KMFSAKAASGTQ 210

RESULT 39

US-08-621-081A-19
; Sequence 19, Application US/08621081A
; Patent No. 5795974
; GENERAL INFORMATION:
; APPLICANT: Cole, Barry C.
; APPLICANT: Atkin, Curtis L.
; APPLICANT: Knudsen, Kevin L.
; APPLICANT: Sawitzke, Allen D.
; TITLE OF INVENTION: Mycoplasma Arthritis Superantigen
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5795974th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM ThinkPad 340
; OPERATING SYSTEM: MS-DOS 6.22
; SOFTWARE: Word Perfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,081A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/165,038
; FILING DATE: December 10, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan J. Howarth
; REGISTRATION NUMBER: 36,553
; REFERENCE/DOCKET NUMBER: T676.CIP/U-1195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801)566-6633
; TELEFAX: (801)566-0750
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 221 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-621-081A-19

Query Match 9.4%; Score 95.5; DB 1; Length 221;
Best Local Similarity 20.9%; Pred. No. 0.26;
Matches 45; Conservative 35; Mismatches 64; Indels 71; Gaps 9;

Db 2 GHHHHHMKLRV-----ENPKAQKHFFQNLNNVVFNNKELEDI- 40

QY 63 LRLSKQAKTVVHFKNKTKRVV-----DLKAGIHTADLINTSDIKAI 103

Db 41 -----YNLSNKESTKEVLKLFKLKVNQFVYRHAFIGVINDYNGLLLEYKEIFNNMFLK-L 91

QY 104 SUNVDTKKQVKDEAKANVQPYTITVNGTSQNILSNITFFKNQIQISYKDIENNVKSVLK 163

Db 92 SVVFDIQR-----KEANNVEQIKENIA-----ILDEIMAKANDLSYFISQN-----K 134

QY 164 SNRGITDVLRLSKQAKFTVNFKNKTKKVIDLKAG 198

Db 135 NFQELDWKAVKLTKEMKIKL---KGQK--LDLRDG 164

RESULT 40

US-09-107-433-3308
; Sequence 3308, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3308:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...331
; SEQUENCE DESCRIPTION: SEQ ID NO: 3308:
US-09-107-433-3308

Query Match 9.4%; Score 95; DB 4; Length 331;
Best Local Similarity 22.9%; Pred. No. 0.51;
Matches 54; Conservative 32; Mismatches 64; Indels 86; Gaps 13;

QY 3 GSHHHHHSQIPYITVNGTSQNILSFLFNKNQIQISYKDIENKVKSVLYFNRI 62

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 10:36:37 ; Search time 168 Seconds

(without alignments)
460.429 Million cell updates/sec

Title: US-10-041-775-2

Perfect score: 1016

Sequence: 1 MRGSHHHHHSQIPYITV.....FTVNFKNGTKKVIDLKAGIY 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003s.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1016	100.0	200	6	ABP58754 Recombina
2	950	93.5	689	2	AAW26301 Staphyloc
3	886.5	87.3	657	6	AAO27181 Staphyloc
4	818.5	80.6	584	6	ABM71428 Staphyloc
5	626	61.6	131	5	AAE25524 Staphyloc
6	626	61.6	131	6	ABP58755 Recombina
7	440	43.3	150	2	AAW89790 Staphyloc
8	210	20.7	144	6	ABM73216 Staphyloc
9	210	20.7	151	2	AAW89785 Staphyloc
10	159	15.6	31	2	AAW26302 Staphyloc
11	155	15.3	31	2	AAW26303 Staphyloc
12	142	14.0	141	6	ABJ19003 Pathogen
13	142	14.0	141	6	ABM73460 Staphyloc
14	135	13.3	96	6	ABM71429 Staphyloc
15	133	13.1	343	7	ABM79016 Staphyloc
16	131	12.9	316	7	ABM79017 Staphyloc
17	117.5	11.6	391	5	ABM79627 Plasmodi
18	117.5	11.6	391	6	ABP71275 E. coli e
19	117.5	11.6	391	2	ADM86524 E. coli e
20	116.5	11.5	512	2	AAW31554 Collagen
21	115	11.3	374	6	ABU44119 Protein e
22	114.5	11.3	393	5	ABB79625 E. coli e
23	114.5	11.3	393	6	ABP71273 P. falcip
24	114.5	11.3	393	7	ADM86520 pET42a Pl
25	114	11.2	211	2	AAW31553 Collagen

ALIGNMENTS

RESULT 1

ABP58754

ID ABP58754 standard; protein; 200 AA.

AC ABP58754;

XX

DT 03-APR-2003 (first entry)

DE Recombinant Staphylococcus aureus Map19.

XX

KW Map19; Map; major histocompatibility complex class II analogue protein; recombinant; T-cell mediated response; prevention; modulation; T-cell overstimulation; toxic shock syndrome; poison ivy; T-cell lymphoproliferative disease; leukaemia; autoimmune disease; delayed-type hypersensitivity response; DTH; staphylococcal infection; immunomodulator; immunosuppressive; cytostatic; vaccine.

OS Staphylococcus aureus.

OS Synthetic.

XX

PN WO200277010-A2.

XX

PD 03-OCT-2002.

XX

PF 10-JAN-2002; 2002WO-US0000401.

XX

PR 10-JAN-2001; 2001US-0260523P.

XX

PA (TEXA) UNIV TEXAS A & M SYSTEM.

XX

PI Brown EN, Lee LY, Hook M;

XX

WPI; 2003-046760/04.

XX

N-PSDB; ABZ25999.

XX

PT New method of preventing or modulating T-cell-mediated response in a host, useful for e.g. the treatment of toxic shock syndrome, comprises administering a Staphylococcus aureus major histocompatibility complex class II analog protein.

XX

PS Claim 7; Page 53; 55pp; English.

XX

CC The invention relates to a novel method of preventing or modulating a T-cell mediated response in an individual involving the administration of the Staphylococcus aureus major histocompatibility complex class II analogue protein (Map), or its active fragments such as Map19 (ABP58754) and Map10 (ABP58755). Map, and its active fragments Map19 and Map10, may be used to treat or prevent pathogenic conditions associated with

CC overstimulation of T-cells such as toxic shock syndrome or poison ivy,
CC and T-cell lymphoproliferative diseases such as leukaemia and autoimmune
CC disease. They may also be used to reduce delayed-type hypersensitivity
CC (DTH) responses and to prevent or modulate a T-cell mediated response to
CC a staphylococcal infection. The present sequence represents recombinant
CC Map19
XX
SQ Sequence 200 AA;

Query Match 100.0%; Score 1016; DB 6; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.8e-80;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGSHHHHSGSQIPYITVNGTSQNLISLTFKKNQOISYKDIENKVKSVLYFNRGISD 60
Db 1 MRGSHHHHSGSQIPYITVNGTSQNLISLTFKKNQOISYKDIENKVKSVLYFNRGISD 60
Qy 61 IDRLSKQAKYTVHFKNGTKRVVDLKGAGHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
Db 61 IDRLSKQAKYTVHFKNGTKRVVDLKGAGHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
Qy 121 NVQVPYITVNGTSQNLISLTFKKNQOISYKDIENKVKSVLYFNRGISD 180
Db 121 NVQVPYITVNGTSQNLISLTFKKNQOISYKDIENKVKSVLYFNRGISD 180
Qy 181 FTVNFKNGTKKVIDLKAGIY 200
Db 181 FTVNFKNGTKKVIDLKAGIY 200

RESULT 2
AAW26301
ID AAW26301 standard; protein; 689 AA.
XX
AC AAW26301;

DT 17-OCT-2003 (revised)
DT 16-NOV-1997 (first entry)
XX
DE Staphylococcal MHC class II antigen analogue protein.
XX
KW MHC II analogue protein; major histocompatibility complex;
KW staphylococcal; adhesin; virulence factor; vaccine.
XX

Staphylococcus aureus; strain FDA 574.

Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= Sig_peptide
FT 31..689
FT /label= Mat_protein

US5648240-A.
XX
XX
PD 15-JUL-1997.
XX
XX
PF 24-MAY-1994; 94US-00248021.
XX
XX
PR 24-MAY-1994; 94US-00248021.
XX
XX
PA (TEXA) UNIV TEXAS A & M.

Jonsson K, Hook M, Patti JM, Gurusiddappa S;
XX
XX WPI; 1997-372059/34.
XX
XX N-PSDB; AAT84441.
XX
FT DNA encoding Staphylococcus aureus broad spectrum adhesin - for
FT production of recombinant adhesin for use in vaccines.
XX
XX Claim 17; Col 11-14; 30pp; English.
XX
XX This protein sequence comprises a broad spectrum adhesin of

CC Staphylococcus aureus FDA 574 that is capable of binding fibronectin or
CC vitronectin and which includes six repeated segments containing MHC II
CC mincing units (see AAW26302-07) of about 30 amino acid residues.
CC Studies of the binding specificities of the adhesin show that it
CC functionally resembles an MHC II antigen in that it binds synthetic
CC peptides. Vectors incorporating DNA (see AAT84441) encoding the adhesin
CC can be used to express recombinant adhesin in transformed host (esp.
CC bacterial, partic. E. coli) cells. Recombinant adhesin can be used in
CC vaccines against staphylococcal infections. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 689 AA;

Query Match 93.5%; Score 950; DB 2; Length 689;
Best Local Similarity 97.0%; Pred. No. 8.3e-74;
Matches 191; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 SHHHHHHSGSQIPYITVNGTSQNLISLTFKKNQOISYKDIENKVKSVLYFNRGISD 63
Db 41 SLHHGYSKIQIPYITVNGTSQNLISLTFKKNQOISYKDIENKVKSVLYFNRGISD 100
Qy 64 RLSKQAKYTVHFKNGTKRVVDLKGAGHTADLINTSDIKAISVNVDTKKQVKDKEAKANVQ 123
Db 101 RLSKQAKYTVHFKNGTKRVVDLKGAGHTADLINTSDIKAISVNVDTKKQVKDKEAKANVQ 160
Qy 124 VPYITVNGTSQNLISLTFKKNQOISYKDIENKVKSVLYFNRGISD 183
Db 161 VPYITVNGTSQNLISLTFKKNQOISYKDIENKVKSVLYFNRGISD 220
Qy 184 NFKNGTKKVIDLKAGIY 200
Db 221 NFKNGTKKVIDLKAGIY 237

RESULT 3
AAO27181
ID AAO27181 standard; protein; 657 AA.
XX
AC AAO27181;

DT 17-SEP-2003 (first entry)
XX
DE Staphylococcus aureus p70 protein, member of the EAP family.
XX

EAP; extracellular adherence protein; antiinflammatory; fibrinogen;
KW ICAM-1; radiation; allergin; sunburn; asthma; psoriasis; encephalitis;
KW meningitis; osteomyelitis; gingivitis; pancreatitis; antiadhesive;
KW cancer therapy; atherosclerosis; rheumatoid arthritis; strain wood 46.
XX

Staphylococcus aureus.

Key Location/Qualifiers
FT Region 22..50
FT /note= "Repeat region 1"
FT Region 131..159
FT /note= "Repeat region 1"
FT Region 332..362
FT /note= "Repeat region 2"
FT Region 437..477
FT /note= "Repeat region 2 with a partial 10 residue overlap
FT of repeat region 1"
FT Region 542..572
FT /note= "Repeat region 2"

WO2003041726-A1.
XX
XX 22-MAY-2003.
XX
XX 14-NOV-2002; 2002WO-SR002075.
XX
XX 16-NOV-2001; 2001SE-00003831.
XX
XX 16-NOV-2001; 2001US-0331456P.
XX
XX 21-NOV-2001; 2001US-0331782P.

XX	PA	(BIOS-) BIOTAPRO AB.	PD	28-NOV-2002.		
XX	XX		PF	27-MAR-2002; 2002WO-IB002637.		
XX	PI	Flock J, Herrmann M, Preisner KT, Chavakis T;	XX			
XX	XX	WPI; 2003-468585/44.	PR	27-MAR-2001; 2001GB-00007661.		
XX	DR		XX	(CHIR-) CHIRON SPA.		
XX	PT	Use of extracellular adherence protein for the manufacture of anti-inflammatory or antitumor drug in the treatment of e.g. atherosclerosis.	XX	Masignani V, Mora M, Scarselli M;		
XX	PS	Disclosure; Page 6; 22pp; English.	XX	WPI; 2003-120786/11.		
XX	CC	This invention relates to the use of extracellular adherence proteins (EAPs) are used for antiinflammatory purposes to treat acute or chronic inflammation. Proteins of the EAP family are produced by the bacterium <i>Staphylococcus aureus</i> (S. aureus) and are able to bind to S. aureus cells and agglutinate them. This invention, however, relates to the ability of EAP to bind adhesive proteins in the connective tissue and on cell surfaces, such that it blocks the inflammatory response of the infected host organism. Specifically EAP can bind fibrinogen in the extracellular matrix or ICAM-1 on cells to inhibit the mobility, infiltration and activities of granulocytes, macrophages and lymphocytes. Note that the inflammatory disorders can be from either a bacterial or non-bacterial source and could include responses to radiation, infection, chemicals, allergins and injury. As such EAP can be used as an antiinflammatory to treat various conditions including sunburn, asthma, allergy, psoriasis, encephalitis, meningitis, osteomyelitis, gingivitis and pancreatitis. Furthermore, the antiadhesive potential of EAP provides a method for cancer therapy and treatment of atherosclerosis and rheumatoid arthritis caused by uncontrolled cellular extravasation of leukocytes. This polypeptide sequence is the <i>Staphylococcus aureus</i> strain Wood 46 p70 protein, which is a typical member of the EAP family of the invention	XX	DR N-PSDB; ACF72988.		
XX	SQ	Sequence 657 AA;	XX	Claim 1; SEQ ID NO 1336; 49pp; English.		
		Query Match 87.3%; Score 886.5; DB 6; Length 657;	CC	The invention relates to novel genes and encoded proteins from <i>Staphylococcus aureus</i> . A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to <i>Staphylococcus bacteria</i> , specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention	CC	PT New <i>Staphylococcus aureus</i> protein, useful as a vaccine for treating or preventing <i>Staphylococcal</i> infection, specifically an infection caused by S. aureus, e.g. sepsis.
		Best Local Similarity 90.8%; Pred. No. 2.6e-68;	CC	Sequence 584 AA;		
		Matches 177; Conservative 8; Mismatches 9; Indels 1; Gaps 1;	XX	Query Match 80.6%; Score 818.5; DB 6; Length 584;		
Qy	6	HHHGHGSGIPTYITVNGTSQNLSTFNKQIQSYKDIENKVSVLVFNRGISIDRL 65	XX	Best Local Similarity 82.3%; Pred. No. 1.8e-62;		
Db	13	HGHSTQIPYITVNGTSQNLSTFNKQIQSYKDIENKVSVLVFNRGISIDRL 72	XX	Matches 163; Conservative 19; Mismatches 15; Indels 1; Gaps 1;		
Qy	66	SKQAKYTVHFKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKKAAKANQVP 125	Qy	4 SHHHHGSQIPTYITVNGTSQNLSTFNKQIQSYKDIENKVSVLVFNRGISIDRL 63		
Db	73	SKQAEYTVHFKNGTKRVVDLKSGTYTADLINTSDIKAISVNVDTKKQPKDK-AKANQVP 131	Db	41 SLHHGSKVHPYAITVNGTSQNLSTFNKQIQSYKDIENKVSVLKSDRGISIDL 100		
Qy	126	YTIIVNGTSQNLSTFNKQIQSYKDIENKVSVLKSNRGITDVLRLSKQAKFTVNF 185	Qy	64 RLSQAKYTVHFKNGTKRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKKAA-KANV 122		
Db	132	YTIIVNGTSQNLSTFNKQIQSYKDIENKVSVLKSNRGITDVLRLSKQAKYTVNF 191	Db	101 RLSQAKYTVYFKNGTKRVVDLKAGIYTDLINTSEIKAININVDTKKQVEDKKDKANY 160		
Qy	186	KNGTKKVIDLKAGIY 200	Qy	123 QVPYITVNGTSQNLSTFNKQIQSYKDIENKVSVLKSNRGITDVLRLSKQAKFT 182		
Db	192	KNGTKKVIDLKAGIY 206	Db	161 QVPYITVNGTSQNLSTFNKQIQSYKDIENKVSVLKSNRGITDVLRLSKQAKY 220		
RESULT 4			Qy	183 VNFKNGTKKVIDLKAGIY 200		
ABM71428			Db	221 VNFKNGTKKVIDLKSGIY 238		
ID	ABM71428	standard; protein; 584 AA.	RESULT 5			
XX	XX		AAE25524			
XX	AC	ABM71428;	ID	AAE25524 standard; protein; 131 AA.		
XX	DT	20-NOV-2003 (first entry)	XX	XX		
XX	DE		XX	AC AAE25524;		
XX	XX	Staphylococcus aureus protein #668.	XX	DT 04-NOV-2002 (first entry)		
XX	KW	Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;	XX	DE Staphylococcus aureus Map10 protein.		
XX	KW	enzymatic assay; antibiotic target.	XX	XX Map10 protein; infection; immunological response; passive immunisation;		
XX	OS		XX	KW vaccine; antibacterial.		
XX	XX	Staphylococcus aureus.	XX	XX Staphylococcus aureus.		
XX	PN	WO200294868-A2.	XX	OS WO200234788-A1.		
XX	XX		XX	PN WO200234788-A1.		
XX	XX		XX	PD 02-MAY-2002.		
XX	XX		XX	XX 22-OCT-2001; 2001WO-US032550.		

XX 20-OCT-2000; 2000US-0241832P.
 PR 21-MAR-2001; 2001US-0277287P.
 XX (INHI-) INHIBITEX INC.
 PA Patti JM, Domanski P, Patel P;
 XX
 PI WPI; 2002-547435/58.
 XX N-PSDB; AAD41844.
 DR
 XX Antibody capable of binding subdomains of Map10 protein, a surface
 PT localized protein from *Staphylococcus aureus*, useful for preventing and
 PT treating staphylococcal infection in humans or animals.
 XX
 XX Claim 28; Page 46-47; 52pp; English.
 XX
 CC The present sequence relates to novel antibodies which are capable of
 CC binding to the subdomains Map10 protein, a surface localised protein from
 CC *Staphylococcus aureus*. Sequences of the invention prevent *S. aureus*
 CC infection in a human or animal and inhibit binding of staphylococcal
 CC bacteria to eukaryotic cells. They are also useful for diagnosing an
 CC infection of *S. aureus* in a sample and for treating or preventing *S. aureus*
 CC infection in humans or animals. Antibodies of the invention are useful
 CC for inducing an immunological response in a human or animal and for
 CC identifying antibodies to the Map10 protein in a sample. They are also
 CC useful in preventing adherence of *Staphylococcal* bacteria, in production
 CC of facilities or laboratories to isolate additional quantities of the
 CC proteins, such as by affinity chromatography and in the development of
 CC vaccines for passive immunisation against staphylococcal infections. The
 CC antibodies prevent or reduce bacterial infection on in-dwelling medical
 CC devices to make them safer to use, including sutures, replacement heart
 CC valves, cardiac assist devices, hard and soft contact lenses, intraocular
 CC lens implants, other implants such as corneal inlays, kerato-protheses,
 CC vascular stents, dental prostheses, pacemakers and heart valves. The
 CC present sequence is *Staphylococcus aureus* Map10 protein
 XX
 XX Sequence 131 AA;

Query Match 61.6%; Score 626; DB 5; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.3e-46;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRGSHHHHGGSQIPYTTVNGTSQNLSSLTFFNKNQISYKDIEKVSVLYFNRGISD 60
 Db 1 MRGSHHHHGGSQIPYTTVNGTSQNLSSLTFFNKNQISYKDIEKVSVLYFNRGISD 60
 Qy 61 IDRLSKQAKYTVHFKNKGTFRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
 Db 61 IDRLSKQAKYTVHFKNKGTFRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
 Qy 121 NV 122
 Db 121 NV 122

RESULT 6
 ABP58755
 ID ABP58755 standard; protein; 131 AA.
 XX
 AC ABP58755;
 XX
 DT 03-APR-2003 (first entry)
 XX
 XX Recombinant *Staphylococcus aureus* Map10.
 XX
 KW Map10; Map; major histocompatibility complex class II analogue protein;
 KW recombinant; T-cell mediated response; prevention; modulation;
 KW T-cell overstimulation; toxic shock syndrome; poison ivy;
 KW T-cell lymphoproliferative disease; leukaemia; autoimmune disease;
 KW delayed-type hypersensitivity response; DTH; staphylococcal infection;
 KW immunomodulator; immunosuppressive; cytostatic; vaccine.
 XX

OS *Staphylococcus aureus*.
 OS Synthetic.
 XX WO200277010-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 10-JAN-2002; 2002WO-US000401.
 XX
 PR 10-JAN-2001; 2001US-0260523P.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX Brown EN, Lee LY, Hook M;
 XX WPI; 2003-046760/04.
 DR N-PSDB; ABZ26000.
 DR
 XX New method of preventing or modulating T-cell-mediated response in a
 PT host, useful for e.g. the treatment of toxic shock syndrome, comprises
 PT administering a *Staphylococcus aureus* major histocompatibility complex
 PT class II analog protein.
 XX
 PS Claim 13; Page 55; 55pp; English.
 XX
 CC The invention relates to a novel method of preventing or modulating a T-
 CC cell mediated response in an individual involving the administration of
 CC the *Staphylococcus aureus* major histocompatibility complex class II
 CC analogue protein (Map), or its active fragments such as Map19 (ABP58754)
 CC and Map10 (ABP58755). Map, and its active fragments Map19 and Map10, may
 CC be used to treat or prevent pathogenic conditions associated with
 CC overstimulation of T-cells such as toxic shock syndrome or poison ivy,
 CC and T-cell lymphoproliferative diseases such as leukaemia and autoimmune
 CC disease. They may also be used to reduce delayed-type hypersensitivity
 CC (DTH) responses and to prevent or modulate a T-cell mediated response to
 CC a staphylococcal infection. The present sequence represents recombinant
 CC Map10
 XX
 XX Sequence 131 AA;

Query Match 61.6%; Score 626; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.3e-46;
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRGSHHHHGGSQIPYTTVNGTSQNLSSLTFFNKNQISYKDIEKVSVLYFNRGISD 60
 Db 1 MRGSHHHHGGSQIPYTTVNGTSQNLSSLTFFNKNQISYKDIEKVSVLYFNRGISD 60
 Qy 61 IDRLSKQAKYTVHFKNKGTFRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
 Db 61 IDRLSKQAKYTVHFKNKGTFRVVDLKAGIHTADLINTSDIKAISVNVDTKKQVKDKEAKA 120
 Qy 121 NV 122
 Db 121 NV 122

RESULT 7
 AAW89790
 ID AAW89790 standard; protein; 150 AA.
 XX
 AC AAW89790;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 XX *Staphylococcus aureus* protein SEQ ID #5238.
 DE
 XX Computer readable medium; vaccine; *S. aureus* infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome.
 KW
 OS *Staphylococcus aureus*.


```
RESULT 12
ABJ19003
ID ABJ19003 standard; protein; 141 AA.
XX
AC ABJ19003;
XX
DT 06-MAR-2003 (first entry)
XX
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 221.
XX
KW Antibacterial; virucide; fungicide; protozoicide; cytostatic; anti-HIV;
KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW autoimmune disease; HIV; hepatitis.
XX
OS Staphylococcus sp.
XX
PN WO200259148-A2.
XX
PD 01-AUG-2002.
XX
PF 21-JAN-2002; 2002WO-EP000546.
XX
PR 26-JAN-2001; 2001AT-00000130.
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvytska O, Etz H, Dryla A, Weichhart T, Hafner M;
PI Tempelmaier B;
XX
DR WPI; 2003-075410/07.
XX
PT Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
PS Example 7; Page 186; 252pp; English.
XX
CC The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against S. aureus or S. epidermidis. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC against S. aureus or S. epidermidis. The antibody preparations or colonisation
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
SQ Sequence 141 AA;
Query Match 14.0%; Score 142; DB 6; Length 141;
Best Local Similarity 33.0%; Pred. No. 0.00018;
Matches 31; Conservative 25; Mismatches 38; Indels 0; Gaps 0;
QY 14 IPYITVNGTSQNLSSITFNKNQOISYKDINKVSVLYFNRGISDIDLRLSKOAKYTV 73
:|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 VPTIISVDGITALHRTYFIFPENKNVLYQEIDSKVKNELASQRGVTTEKINNAQTATYTL 106
:|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 74 HFKNKGRKRVLDKAGIHTADLINTSDIKAISVNV 107
:|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 TLNDGNKKVNLKKNDDAKNSIDPSTIKQIIVV 140
:|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 14
ABM71429
ID ABM71429 standard; protein; 96 AA.
XX
AC ABM71429;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus protein #2700.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001GB-00007661.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
DR WPI; 2003-120786/11.
XX
DR N-PSDB; ACF75020.
XX
PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
PT S. aureus, e.g. sepsis.
XX
PS Claim 1; SEQ ID NO 5400; 49pp; English.
XX
CC The invention relates to novel genes and encoded proteins from
CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
CC nucleic acid encoding the protein, or an antibody to the protein, is
CC useful as a pharmaceutical, particularly as a vaccine for treating or
CC preventing infection due to Staphylococcus bacteria, specifically an
CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention
XX
SQ Sequence 141 AA;
Query Match 14.0%; Score 142; DB 6; Length 141;
Best Local Similarity 33.0%; Pred. No. 0.00018;
Matches 31; Conservative 25; Mismatches 38; Indels 0; Gaps 0;
QY 14 IPYITVNGTSQNLSSITFNKNQOISYKDINKVSVLYFNRGISDIDLRLSKOAKYTV 73
:|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 VPTIISVDGITALHRTYFIFPENKNVLYQEIDSKVKNELASQRGVTTEKINNAQTATYTL 106
:|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 74 HFKNKGRKRVLDKAGIHTADLINTSDIKAISVNV 107
:|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 TLNDGNKKVNLKKNDDAKNSIDPSTIKQIIVV 140
:|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 14
ABM71429
ID ABM71429 standard; protein; 96 AA.
XX
AC ABM71429;
XX
DT 20-NOV-2003 (first entry)
```


XX PD 18-SEP-2003.

XX PF 05-MAR-2003; 2003WO-US006415.

XX PR 05-MAR-2002; 2002US-0361324P.

XX PA (INHI-) INHIBITEX INC.

XX PI (TEXA) UNIV TEXAS A & M SYSTEM.

XX PI Patti JW, Hutchins JT, Hall A, Domanski P, Patel P, Hook M; Robbins J, Vernachio J, Bowden MG;

XX PR WPI; 2003-722324/68.

XX DR N-PSDB; ACF80626.

XX

PT New antibody recognizing a Staphylococcus epidermidis protein comprising SdrG N1N2N3, SdrG N2N3 or SdrGR2 useful for preparing a composition for treating or preventing a coagulase-negative Staphylococcal infection.

PT

XX Claim 27; Page 26; 78pp; English.

PS

CC The present sequence comprises the protein sequence of the TR2 protein (amino acids 273-577) of the SdrG surface protein of coagulase-negative Staphylococcus epidermidis. A claimed antibody recognises a protein selected from SdrG N1N2N3, N2N3 and TR2. The antibody may be a monoclonal antibody, including a chimeric, murine, humanized, human or single chain monoclonal antibody, which prevents a coagulase-negative staphylococcal infection in a human or animal by inhibiting binding of staphylococcal bacteria to fibrinogen. Such antibodies can be used to treat or prevent staphylococcal infections including nosocomial coagulase-negative staphylococcal infections in low birth weight infants. A claimed vaccine comprises the isolated SdrG N1N2N3, N2N3 or TR2 protein

XX

SQ Sequence 316 AA;

Query Match 12.9%; Score 131; DB 7; Length 316;

Best Local Similarity 22.6%; Pred. No. 0.0049;

Matches 53; Conservative 33; Mismatches 71; Indels 78; Gaps 9;

QY 1 MRGSHHHHHSQ-----IPYITVNGTS-----QNILSLTFNKNQOI 39

DB 1 MRGSHHHHHSQSGSNVHLKVTQDSITGEGYDSDGIIKAHDAENLIYVTF----- 54

QY 40 SYKDIENKVS-----VLYFNRGISIDL-----RLSKQAKYT 72

DB 55 ---EYDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKDNGSEIATGTYDNTNKQITVT 111

QY 73 VHFKNGTKRVDLKGAIHTADLINTSDIKAISVNVDTKKQYKDKAKANQVPIITVNG 132

DB 112 --FTDYVDKYENIKAKHLKLTSYIDKSKVP-----NNNTKLDVEYKTALSSVNKTIITVEYQK 165

QY 133 TSQNILSLTF-----KKNQOIS-----YKDLNNKVSVLKSNRGITDVD 172

DB 166 PNEKNTANLQSNFTNIDTKNHTVEQTIYNPLRYSAKETNVNISNGDEGSTIID 220

RESULT 17

ID ABB79627

XX ABB79627 standard; protein; 391 AA.

XX

AC ABB79627;

XX

XX 21-OCT-2002 (first entry)

XX

XX Plasmodium falciparum MSP-1(42) recombinant protein.

XX

KW Merozoite surface protein-1; MSP-1; malaria; vaccine; protozoacide.

XX

OS Plasmodium falciparum.

OS Synthetic.

OS Chimeric.

XX

XX Key Location/Qualifiers

FT Peptide 1..17

FT Protein /note= "(His)6 tag and flexible linker peptide"

FT 18..391

XX /note= "MSP-1(42)"

XX WO200258727-A2.

XX

XX 01-AUG-2002.

XX

XX 25-JAN-2002; 2002WO-US002554.

XX

XX 26-JAN-2001; 2001US-0264535P.

XX

XX (REED-) REED ARMY INST RES WALTER.

XX

XX Lyon JA, Angov E, Cohen JD, Voss G;

XX WPI; 2002-590798/63.

XX DR N-PSDB; ABN84474.

XX

PT New vaccine comprising Plasmodium falciparum MSP-142 protein and an adjuvant, useful against malaria or for eliciting immune responses against P. falciparum.

PT

XX Disclosure; Page 98-99; 99pp; English.

XX

CC The present sequence is that of a recombinant protein comprising the Plasmodium falciparum 3b7 merozoite surface protein-1 42 kDa fragment (MSP-1(42)) with an N-terminal (His)6 tag and linker. Recombinant PSP-1(42) protein was produced as a soluble protein in Escherichia coli host cell cytoplasm by manipulation of IPTG concentration and induction temperature. MSP-1(42) was purified to greater than 95% purity, and showed immunoreactivity with anti-MSP-1 antibodies. It was stable when stored for 18 months at -80 degrees C. The invention relates to the production of large amounts of MSP-1(42) which maintain conformational epitopes critical for development of vaccines. The vaccines are useful against malaria or for eliciting immune responses against P. falciparum. The recombinant MSP-1(42) proteins are useful in diagnostic assays, for in vitro monitoring of malaria infection or prognosing the response to treatment of malaria patients, and for production of antibodies used for malaria antigen detection or as therapeutic or prophylactic agents

XX

SQ Sequence 391 AA;

Query Match 11.6%; Score 117.5; DB 5; Length 391;

Best Local Similarity 22.2%; Pred. No. 0.099;

Matches 52; Conservative 34; Mismatches 91; Indels 57; Gaps 9;

QY 4 SHHHHHH-GSQIPYITVNGTSQNILSLTFNKNQOISY-----KDIENKVS 50

DB 2 AHHHHHPGSGSGTMAISVTMDNILSG--FENEYDVIYKPLAGVYRSLKKQIE---KN 56

QY 51 VLYFNRGISIDLRLSKQAKYTVHFKNGTKRVDLKGAIHTADLINTSDIKAISVNVDTK 110

DB 57 IFTNLNLDILNRLKKRYFL-----DVLESDLMQFKHISSEYIIDS 102

QY 111 KQVKDKAKANQVPIITVNGTSQNI---LSNLTFFKNQOISYKDLNNKVSVLKSNR- 166

DB 103 FKLLNSEQNTLLSKYKIKESVENDIKFAQEGISYVEKVLAKYKDDLESIKKVEEKE 162

QY 167 -----GITVDVLDRLSKQAKFTVN-----FRNGTKKV-----IDLKAGI 199

DB 163 KFPSSPPTPPSPAKTDEQKESKFLPFLTNIETLYNNLVNKNIDYDLINLAKI 216

RESULT 18

ID ABB71275

XX ABB71275 standard; protein; 391 AA.

XX

AC ABB71275;

XX

XX 28-APR-2003 (first entry)

XX E. coli expressed P. falciparum MSP1_42 (3D7) protein sequence.
DE
KW MSP-1_42; merozoite protein; protozoacide; vaccine; malaria; mosquito.
XX Plasmodium falciparum.
XX WO2003004525-A2.
XX 16-JAN-2003.
XX 25-JAN-2002; 2002WO-US002428.
XX 29-JAN-2001; 2001US-0264535P.
XX 26-OCT-2001; 2001US-0347564P.
XX (REED-) REED ARMY INST RES WALTER.
XX Lyon JA, Angov E;
XX WPI; 2003-221577/21.
XX New recombinant Plasmodium falciparum merozoite protein (MSP)-142 which
PT retains its native folding, useful for detecting and preventing malaria
PT infection, and for antibody production.
XX Disclosure; Page 103; 104pp; English.
XX The invention relates to a recombinant Plasmodium falciparum merozoite
CC protein, (MSP)-142 which retains its native folding. The protein is
CC useful as a diagnostic reagent, in antibody production, and as a vaccine
CC against malaria. The antibody may also be used for detecting and treating
CC chronic malaria infection. The present sequence represents a recombinant
CC E. coli expressed P. falciparum MAP-1_42 protein
XX
SQ Sequence 391 AA;
Query Match 11.6%; Score 117.5; DB 6; Length 391;
Best Local Similarity 22.2%; Pred. No. 0.099;
Matches 52; Conservative 34; Mismatches 91; Indels 57; Gaps 9;
QY 4 SHHHHHH-GSQIPYITVNGTSQNLSSLTFFKNQOISY-----KDLENKVK 50
DB 2 AHHHHHPGGSGGTMAISVTMDNLG--FENEYDVIYKPLAGVYRSKKQIE--KN 56
QY 51 VLYFNRGISDIDLRLSKQAKYTVHFKNKTRVVDLKGHTADLINTSDIKAISVNVDTK 110
DB 57 IFTNLLNLDILNLSRLKRRKYFL-----DVLESQDLMPKHSSNEVYIIDS 102
QY 111 KOVKDKKAKANVQVPYITVNGTSQNI---LSNLTFFKNQOISYKDLNNVSKVLKSNR- 166
DB 103 FKLLNSEQKNTLLSKYKIKESVENDIKFAQEGISYVEKVLAKYKDDLESIKKVIKEKE 162
QY 167 -----GITDVLRLSKQAKFTVN----FKNGTKKV----IDLKAGI 199
DB 163 KFPSSPPTTPSPAKTDEQKESKFLPFLNTIETLYNNLVNKIDDDYLINLAKI 216
RESULT 19
ADM86524
ID ADM86524 standard; protein; 391 AA.
XX ADM86524;
XX 03-JUN-2004 (first entry)
XX E. coli expressed Plasmodium falciparum MSP142 (3D7) protein.
XX Malaria; vaccine; merozoite surface protein-142; MSP-142;
KW immune response; diagnosis.
XX Plasmodium falciparum.
XX

PN US2003161839-A1.
XX 28-AUG-2003.
XX 25-JAN-2002; 2002US-00057532.
XX 29-JAN-2001; 2001US-0264535P.
XX 26-OCT-2001; 2001US-0347563P.
XX (LYON/) LYON J A.
XX (ANGOV/) ANGOV E.
XX (COHEN/) COHEN J D.
XX (VOSS/) VOSS G.
XX Lyon JA, Angov E, Cohen JD, Voss G;
XX WPI; 2003-843522/78.
XX N-PSDB; ADM86523.
XX Malaria vaccine comprises Plasmodium falciparum merozoite surface protein
PT -142.
XX Disclosure; SEQ ID NO 7; 41pp; English.
XX The invention relates to a malaria vaccine which comprises Plasmodium
CC falciparum merozoite surface protein-142 (MSP-142), and an adjuvant
CC consisting of A, B, C, D, and E. The invention also relates to a method
CC for inducing protective immune response to malaria. The invention is used
CC as diagnostic reagent for antibody production or as vaccine against
CC malaria infection. The present sequence is E. coli expressed P.
CC falciparum MSP142 (3D7) protein. This sequence is used to illustrate the
CC method of the invention.
XX
SQ Sequence 391 AA;
Query Match 11.6%; Score 117.5; DB 7; Length 391;
Best Local Similarity 22.2%; Pred. No. 0.099;
Matches 52; Conservative 34; Mismatches 91; Indels 57; Gaps 9;
QY 4 SHHHHHH-GSQIPYITVNGTSQNLSSLTFFKNQOISY-----KDLENKVK 50
DB 2 AHHHHHPGGSGGTMAISVTMDNLG--FENEYDVIYKPLAGVYRSKKQIE--KN 56
QY 51 VLYFNRGISDIDLRLSKQAKYTVHFKNKTRVVDLKGHTADLINTSDIKAISVNVDTK 110
DB 57 IFTNLLNLDILNLSRLKRRKYFL-----DVLESQDLMPKHSSNEVYIIDS 102
QY 111 KOVKDKKAKANVQVPYITVNGTSQNI---LSNLTFFKNQOISYKDLNNVSKVLKSNR- 166
DB 103 FKLLNSEQKNTLLSKYKIKESVENDIKFAQEGISYVEKVLAKYKDDLESIKKVIKEKE 162
QY 167 -----GITDVLRLSKQAKFTVN----FKNGTKKV----IDLKAGI 199
DB 163 KFPSSPPTTPSPAKTDEQKESKFLPFLNTIETLYNNLVNKIDDDYLINLAKI 216
RESULT 20
AAW31554
ID AAW31554 standard; protein; 512 AA.
XX AAW31554;
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 21-MAY-1998 (first entry)
XX Collagen binding protein M55 epitope.
XX Collagen binding protein; cna gene; sepsis; infection;
KW microbial surface component regionising adhesive matrix molecule; MSCRAMM;
KW adhesin; vaccine; immunisation; diagnosis; therapy; epitope M55.
XX Staphylococcus aureus.

```
XX Key Location/Qualifiers
FH Peptide 1. .12
FT Protein /note= "vector pQE30-derived peptide"
FT Protein 13. .512
FT Protein /note= "epitope M17"
XX
XX WO9743314-A2.
XX
XX 20-NOV-1997.
XX
XX 14-MAY-1997; 97WO-US008210.
XX
XX 16-MAY-1996; 96US-0017678P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX (UABR-) UAB RES FOUND.
XX
XX Hoeek M, Patti JM, House-Pompeo K, Schanam N, Symersky J;
XX
XX WPI; 1998-008801/01.
XX N-PSDB; AAT93438.
XX
XX Antibody that interacts with collagen binding domain of Staphylococcal
XX cna gene product - useful to prevent bacterial sepsis in animal infected
XX with Staphylococcus aureus.
XX
XX Claim 31; Page 117-119; 143pp; English.
XX
XX This protein comprises Staphylococcus aureus collagen binding protein
XX (CBP) epitope M55, i.e. amino acids 30-531 of full-length CBP, plus a
XX vector-derived N-terminal peptide. Claimed 441, 849 and 1500 bp nucleic
XX acid sequences (see AAT93436-38) respectively encode CBP epitopes M17,
XX M31 and M55 (see AAW31552-54) that confer protection against S. aureus
XX infection. These nucleic acid sequences can be used in the recombinant
XX production of the CBP epitopes. The CBP protein and antigenic epitopes
XX are contemplated for use in the treatment of pathological infections,
XX especially to prevent bacterial adhesion to collagen. The claimed nucleic
XX acids as well as claimed anti-CBP antibodies will also be of use in
XX screening, diagnostic and therapeutic applications including active and
XX passive immunisation and methods for the prevention of bacterial
XX colonisation in an animal such as a human. The CBP epitopes are also
XX contemplated for use in the preparation of vaccines and as carrier
XX proteins in vaccine formulations, as well as in the formulation of
XX compositions for the prevention of S. aureus infection. (Updated on 25-
XX MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
XX field.)
XX
XX Sequence 512 AA;
XX
XX Query Match 11.5%; Score 116.5; DB 2; Length 512;
XX Best Local Similarity 23.8%; Pred. No. 0.17;
XX Matches 64; Conservative 29; Mismatches 79; Indels 97; Gaps 14;
XX
XX QY 1 MRGSHHHHGGGQIPYITVNGTSQNILSS-----LTF-NKQQQISYKD----- 43
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 MRGSHHHHGGGARDISST-NVTDLTVSFSGKIEDGGKTVKMTFDDKNGKIQNGDMIKVA 59
XX
XX QY 44 -----IENKVKSV-----LYFN-----RGISDLDLRLSKOAKY 72
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 60 WPTSTGVKIEGSKVPLTVKGEQGVQAVITPDGATITFNDKVEKLSDV-----SGFAFFE 115
XX
XX QY 73 VHFKNKTKRVVDLKGAGHTADLINTSDIKAISV---NVDTKQVKDKKA----- 118
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 116 VQGRNLQ-----TNTSDDKVATITSGNKSNTVTVHKSEAGTSVFYKGTG 161
XX
XX QY 119 -----KANQVQPVYITVNGTSQNILNLFKK-----NQQISYKDLNNV-----KSVLKSNR 166
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 162 DMLPDDTTHVRWFLNINNEKSYVSKDITIKQIQGGQQLDLSTLINTVGTSHSNYSGQS 221
XX
XX QY 167 GTTVDLRLSKOAKFTVNFKNKTKKVIDL 195
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 222 AITDFE-KAFPGSKITV---DNTRKTIIV 246
```

RESULT 21

ABU44119

ID ABU44119 standard; protein; 374 AA.

XX AC ABU44119;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #29646.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Streptococcus mutans.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA47989.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 72043; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

```
XX SQ Sequence 374 AA;
Query Match 11.3%; Score 115; DB 6; Length 374;
Best Local Similarity 24.2%; Pred. No. 0.15;
Matches 52; Conservative 42; Mismatches 63; Indels 58; Gaps 13;
QY 18 ITVNGTSQNLSTFNKQOISYKDINKVSVLY----FNKGISDIDLRLSKQAKYTV 73
Db 131 ITVSGNKNAIESQLI----BELGIKK-SDYLTLLFOANFRFNLSKSD-KWVKEAKLVY 184
QY 74 HFKNQ-TKRVD-----LKAGIHTADLINTSDIKA--ISVNVDTKKQVK 114
Db 185 HFPNHFTRVKEVRIIAYRQTDKGYVPILENGTR-VDTVNASELPGSFVTINLDOEKEVR 243
QY 115 -----DKEAKANVQVPIITVNGTSONILSTFNKQOISYKDLNENKSVLKS 165
Db 244 ELVQKLAKLDKSLVGSIKV--ISSVNSSSTKDLLLEMKDN-----NSRVPL--- 289
QY 166 RGTVDLRLSKQAKFTVNFKNGTKKVIDLKAGIY 200
Db 290 ---SEIDTKLPYYSIKKNTDGS--IVDMVGIIY 319

RESULT 22
ABB79625
ID ABB79625 standard; protein; 393 AA.
AC ABB79625;
XX
XX
DT 21-OCT-2002 (first entry)
XX
DE E. coli expressed P. falciparum MSP-1 recombinant protein.
XX
KW Merozoite surface protein-1; MSP-1; malaria; vaccine; protozoacide.
XX
OS Plasmodium falciparum.
OS Synthetic.
OS Chimeric.
XX
XX WO200258727-A2.
XX
XX PD 01-AUG-2002.
XX
XX PF 25-JAN-2002; 2002WO-US002554.
XX
XX PR 26-JAN-2001; 2001US-0264535P.
XX
XX PA (REED-) REED ARMY INST RES WALTER.
XX
XX PI Lyon JA, Angov E, Cohen JD, Voss G;
XX
XX WPI; 2002-590798/63.
XX
XX New vaccine comprising Plasmodium falciparum MSP-142 protein and an
PT adjuvant, useful against malaria or for eliciting immune responses
PT against P. falciparum.
XX
XX PS Disclosure; Page 92-93; 99pp; English.
XX
XX The present sequence is that of a recombinant protein comprising
CC Plasmodium falciparum 3D7 merozoite surface protein-1 42 kDa fragment
CC (MSP-1(42)) with an N-terminal (His)6-tag for affinity purification and 3
CC linker amino acids. The levels of expression of the recombinant protein,
CC encoded by plasmid pT-IEGR-42(AT), were 2-5% of total E. coli protein,
CC and the protein was correctly folded based on immunoreactivity with a
CC series of MSP-1(19) specific monoclonal antibodies. The present invention
CC relates to the production of large amounts of MSP-1(42) which maintain
CC conformational epitopes critical for development of vaccines. The
CC vaccines are useful against malaria or for eliciting immune responses
CC against P. falciparum. The recombinant MSP-1(42) proteins are useful in
CC diagnostic assays, for in vitro monitoring of malaria infection or
CC prognosing the response to treatment of malaria patients, and for

XX production of antibodies used for malaria antigen detection or as
CC therapeutic or prophylactic agents
XX
XX SQ Sequence 393 AA;
Query Match 11.3%; Score 114.5; DB 5; Length 393;
Best Local Similarity 22.5%; Pred. No. 0.18;
Matches 53; Conservative 34; Mismatches 90; Indels 59; Gaps 10;
QY 4 SHHHHHH-GSQIP--YITVNGTSONILSTFNKQOISY-----KDIENKV 48
Db 2 AHHHHHHPGGSGIEGRGTMAISVTMDNILSG--FENEYDVLYLPLAGVYRSLKKQIE--- 56
QY 49 KSVLYFNRGIDIDLRLSKQAKYTVHFKNGTKRVDLKAGIHTADLINTSDIKAISVNV 108
Db 57 KNITFNLNLDIILNSRLKKRYFL-----DVLESDLMQPKHISSENYIIE 102
QY 109 TKQVKQKQKAKANVQVPIITVNGTSONI---LSNLTFKKNQOISYKDLNENKSVLKS 165
Db 103 DSFKLLNSEQNTLLKSYKIKESVENDIKFAQEGISYVEKVLAKYKDDLESIKKVIKEE 162
QY 166 R-----GITDVLRLSKQAKFTVN----FKNGTKKV----IDLKAGI 199
Db 163 KEKFPSSPPTTPSPAKTDEQKESKFLPLTNIETLYNLDVNLVKNIDYILNLRKAKI 218

RESULT 23
ABB71273
ID ABB71273 standard; protein; 393 AA.
XX
XX AC ABB71273;
XX
XX DT 28-APR-2003 (first entry)
XX
DE P. falciparum MSP1_42 (3D7) protein sequence in clone pET42A.
XX
XX KW MSP-1_42; merozoite protein; protozoacide; vaccine; malaria; mosquito.
XX
XX OS Plasmodium falciparum.
XX
XX PN WO2003004525-A2.
XX
XX PD 16-JAN-2003.
XX
XX PF 25-JAN-2002; 2002WO-US002428.
XX
XX PR 29-JAN-2001; 2001US-0264535P.
XX
XX PR 26-OCT-2001; 2001US-0347584P.
XX
XX PA (REED-) REED ARMY INST RES WALTER.
XX
XX PI Lyon JA, Angov E;
XX
XX WPI; 2003-221577/21.
XX
XX New recombinant Plasmodium falciparum merozoite protein (MSP)-142 which
PT retains its native folding, useful for detecting and preventing malaria
PT infection, and for antibody production.
XX
XX PS Disclosure; Page 96-97; 104pp; English.
XX
XX The invention relates to a recombinant Plasmodium falciparum merozoite
CC protein, (MSP)-142 which retains its native folding. The protein is
CC useful as a diagnostic reagent, in antibody production, and as a vaccine
CC against malaria. The antibody may also be used for detecting and treating
CC chronic malaria infection. The present sequence represents a recombinant
CC E. coli expressed P. falciparum MAP-1_42 protein expressed in clone
CC pET42A
XX
XX SQ Sequence 393 AA;
Query Match 11.3%; Score 114.5; DB 6; Length 393;
Best Local Similarity 22.5%; Pred. No. 0.18;
```


CC hmWB and hmWC genes. The hmWA genes encode the structural HMWA proteins
CC and the hmWB and hmWC genes encode accessory proteins which are
CC responsible for post-translational processing and secretion of the HMWA
CC proteins. The modified hmWABC operon used in the expression construct of
CC the invention contains an A gene modified such that it encodes only the
CC mature HMWA. The invention also discloses hmWA genes (AA52175-A52198)
CC and HMWA proteins (AAB01824-B01849) from the non-typeable H. influenzae
CC strains JcyC, K1, K21, LCDC2, PMH1, 15 and 12. The nucleic acids and
CC vectors are used for the production of recombinant H. influenzae HMW
CC proteins which can be used as vaccines to mediate a humoral or cell-
CC mediated immune response to provide protection against diseases in humans
CC caused by H. influenzae (e.g., otitis media, epiglottitis, pneumonia and
CC tracheobronchitis). The HMW proteins are also useful as antigens in
CC immunoassays for detecting antibodies against Haemophilus, HMW proteins
CC and/or HMW peptides. The nucleotide sequences encoding the HMW proteins
CC can be used to isolate and clone hmw genes from other non-typeable
CC strains of Haemophilus via hybridisation reactions. The present sequence
CC represents a mature HMWA protein from a non-typeable strain of H.
CC influenzae. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 1221 AA;
Query Match 10.8%; Score 110; DB 3; Length 1221;
Best Local Similarity 23.7%; Pred. No. 2.1;
Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;
QY 3 GSHHHHHGSGIPYTI-----TVNGTSQNILSSLTFFNKNQOISYKDIEKNVKS 51
DB 422 GSDFDNH---QKPLTIKDVINSNLTAGGNVINGNLTGVNNGANL--KAITNFTFN 476
QY 52 --LYFNRGISDIDLRLSKQAKYTVHFNGTKRVVDLKAGIHTADLINTSDIKAISVND 109
DB 477 GGLFDNKGNSNISI-----ARGGAKFKDINNNTSSLN--ITTNSDT 514
QY 110 KKQ-----VKDKEAKANVQVPYTI-----TVNGTSQNILSSLTFFNKN 145
DB 515 TYRTIIEGNTNKAAGDLNIDNKGNAEIQIGNISQKEGNTLTISSDKININQITIKGV 574
QY 146 NQOISYKDLNENKSVLKSNGRIGITDVLRLSKQAKFTVNFNGTKKVI 193
DB 575 NKEDSDSTANNANLTIKTKELQTLGDLNISGFDKAEITAKEGADLII 622
RESULT 33
ID AAB01824
XX AAB01824 standard; protein; 1227 AA.
AC AAB01824;
XX 12-SEP-2003 (revised)
DT 11-SEP-2000 (first entry)
XX Haemophilus influenzae strain JcyC HMWA protein, SEQ ID NO:26.
DE
XX HMW protein; hmw gene; hmWA1; hmWA2; high molecular weight;
KW non-typeable Haemophilus influenzae; NTHi; non-encapsulated;
KW recombinant production; Escherichia coli; antibacterial; vaccine;
KW human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
KW detection; diagnosis.
XX
OS Haemophilus influenzae; strain JcyC.
XX
XX WO2000020609-A2.
PN
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-CA000938.
XX
XX 07-OCT-1998; 98US-00167568.
PR 08-DEC-1998; 98US-00206942.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX

PI Loosmore SM, Yang Y, Klein MH;
XX WPI; 2000-303789/26.
DR N-PSDB; AA52175.
XX
XX Nucleic acid molecule for producing recombinant high molecular weight
PT proteins of Haemophilus which are used as a vaccine to provide protection
PT against Haemophilus induced diseases in humans.
XX
XX Claim 12; Fig 18A-R; 307pp; English.
PS
XX The invention relates to the recombinant production of Haemophilus
CC influenzae high molecular weight (HMW) proteins in Escherichia coli. The
CC expression construct used to effect recombinant expression comprises a
CC promoter functional in E. coli (e.g., the T7 promoter) operably linked to
CC a modified hmWABC operon from a non-typeable (non-encapsulated) H.
CC influenzae (NTHi). Most HMW-expressing NTHi strains contain two hmw gene
CC clusters termed hmWA and hmWB. Each hmWABC operon comprises hmWA,
CC hmWB and hmWC genes. The hmWA genes encode the structural HMWA proteins
CC and the hmWB and hmWC genes encode accessory proteins which are
CC responsible for post-translational processing and secretion of the HMWA
CC proteins. The modified hmWABC operon used in the expression construct of
CC the invention contains an A gene modified such that it encodes only the
CC mature HMWA. The invention also discloses hmWA genes (AA52175-A52198)
CC and HMWA proteins (AAB01824-B01849) from the non-typeable H. influenzae
CC strains JcyC, K1, K21, LCDC2, PMH1, 15 and 12. The nucleic acids and
CC vectors are used for the production of recombinant H. influenzae HMW
CC proteins which can be used as vaccines to mediate a humoral or cell-
CC mediated immune response to provide protection against diseases in humans
CC caused by H. influenzae (e.g., otitis media, epiglottitis, pneumonia and
CC tracheobronchitis). The HMW proteins are also useful as antigens in
CC immunoassays for detecting antibodies against Haemophilus, HMW proteins
CC and/or HMW peptides. The nucleotide sequences encoding the HMW proteins
CC can be used to isolate and clone hmw genes from other non-typeable
CC strains of Haemophilus via hybridisation reactions. The present sequence
CC represents an HMWA protein from a non-typeable strain of H. influenzae.
CC (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 1227 AA;
Query Match 10.8%; Score 110; DB 3; Length 1227;
Best Local Similarity 23.7%; Pred. No. 2.1;
Matches 54; Conservative 28; Mismatches 82; Indels 64; Gaps 9;
QY 3 GSHHHHHGSGIPYTI-----TVNGTSQNILSSLTFFNKNQOISYKDIEKNVKS 51
DB 428 GSDFDNH---QKPLTIKDVINSNLTAGGNVINGNLTGVNNGANL--KAITNFTFN 482
QY 52 --LYFNRGISDIDLRLSKQAKYTVHFNGTKRVVDLKAGIHTADLINTSDIKAISVND 109
DB 483 GGLFDNKGNSNISI-----ARGGAKFKDINNNTSSLN--ITTNSDT 520
QY 110 KKQ-----VKDKEAKANVQVPYTI-----TVNGTSQNILSSLTFFNKN 145
DB 521 TYRTIIEGNTNKAAGDLNIDNKGNAEIQIGNISQKEGNTLTISSDKININQITIKGV 580
QY 146 NQOISYKDLNENKSVLKSNGRIGITDVLRLSKQAKFTVNFNGTKKVI 193
DB 581 NKEDSDSTANNANLTIKTKELQTLGDLNISGFDKAEITAKEGADLII 628
RESULT 34
ID ABP39160
XX ABP39160 standard; protein; 288 AA.
AC ABP39160;
XX
XX 24-JUL-2002 (first entry)
DT
XX Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4005.
DE
XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy.
KW

XX OS	Staphylococcus epidermidis.	XX FN	US2004147734-A1.
XX PN	US6380370-B1.	XX PD	29-JUL-2004.
XX XX	30-APR-2002.	XX PF	01-DEC-2003; 2003US-00724972.
XX PD	13-AUG-1998; 98US-00134001.	XX XX	08-NOV-1997; 97US-0064964P.
XX PF	14-AUG-1997; 97US-0055779P.	XX PR	13-AUG-1998; 98US-00134001.
XX PR	08-NOV-1997; 97US-0064964P.	XX PR	29-NOV-1999; 99US-00450969.
XX XX	(GENO-) GENOME THERAPEUTICS CORP.	XX XX	(DOUC/) DOUCETTE-STAMM L.
XX PA	Doucette-Stamm LA, Bush D;	XX PA	(BUSH/) BUSH D.
XX PI	WPI; 2002-381255/41.	XX PI	Doucette-Stamm L, Bush D;
XX XX	N-PSDB; ABN91705.	XX DR	WPI; 2004-580138/56.
XX DR	Novel isolated nucleic acid encoding a Staphylococcus epidermis	XX DR	N-PSDB; ADS03582.
XX XX	polypeptide, useful for diagnosing and treating bacterial infections.	XX PT	New isolated polypeptide and encoding nucleic acid derived from
XX PT	polypeptide, useful for diagnosing and treating bacterial infections.	XX PT	Staphylococcus epidermidis, useful for diagnosing, preventing and/or
XX XX	Disclosure; SEQ ID NO 4005; 267pp; English.	XX PT	treating an S. epidermidis bacterial infection.
XX PS	Disclosure; SEQ ID NO 4005; 267pp; English.	XX XX	Claim 17; SEQ ID NO 6649; 741pp; English.
XX XX	ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading	XX PS	Claim 17; SEQ ID NO 6649; 741pp; English.
XX CC	frame (ORF) nucleic acid sequences which encode the amino acid sequences	XX CC	The invention describes an isolated nucleic acid comprising a nucleotide
XX CC	given in ABP35124 to ABP37960. The S. epidermidis sequences have	XX CC	sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
XX CC	antibacterial activity and can be used in gene therapy. The sequences can	XX CC	1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
XX CC	also be used in the diagnosis and treatment of bacterial infections,	XX CC	of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
XX CC	particularly S. epidermidis infections. The sequences can be used to	XX CC	given in the specification. Also described are: a recombinant expression
XX CC	screen for compounds able to interfere with the S. epidermidis life cycle	XX CC	vector; a cell comprising a recombinant expression vector of (1);
XX CC	or inhibit S. epidermidis infection. N.B. The sequence data for this	XX CC	producing an S. epidermidis polypeptide; an isolated nucleic acid
XX CC	patent did not form part of the printed specification, but was obtained	XX CC	comprising a nucleotide sequence of at least 8 nucleotides in length; a
XX CC	in electronic format directly from the USPTO web site	XX CC	vaccine composition for prevention or treatment of an S. epidermidis
XX XX	Sequence 288 AA;	XX CC	infection, comprising a nucleic acid cited above and a carrier; treating
XX SQ	Sequence 288 AA;	XX CC	a subject for S. epidermidis infection; a recombinant or substantially
	Query Match 10.7%; Score 108.5; DB 5; Length 288;	XX CC	pure preparation of an S. epidermidis polypeptide or its fragment; a
	Best Local Similarity 20.6%; Pred. No. 0.4;	XX CC	vaccine composition for prevention or treatment of an S. epidermidis
	Matches 44; Conservative 43; Mismatches 78; Indels 49; Gaps 6;	XX CC	infection; detecting the presence of a Staphylococcus nucleic acid in a
		XX CC	sample; a computer readable medium having recorded in it the nucleotide
Qy	9 HGSQIPYITVNGTSQNILSLTFNKNQOISYKDIEKNVKSVLVFNRGISDIDLRLSKQ 68	XX CC	sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
Db	28 NNGKKVTIGVASNDTK-----AWEKVKELAKKD-----DIDLEIKHF 64	XX CC	system for identifying fragments of the Staphylococcus genome of
Qy	69 AKYTVHFKNGTKRVVDLKAGIHTA-----DLINTSDIKAISVNVDTKKQVK 114	XX CC	commercial importance; a computer based system for identifying fragments
Db	65 SDYVNPKNALSDGIDIDLNAFQHFALDQYKKAHDTNIEALSTTVLAPLGIYSKVKNIK 124	XX CC	of the Staphylococcus plasmids of commercial importance; identifying
Qy	115 DKEAKANYQVPTITVNGTSQNILSN---LTFKKNQOI--SYKOLENNVKSV-----L 162	XX CC	commercially important nucleic acid fragments of the Staphylococcus
Db	125 DVKGAQVAIPNDVSNQARALKLLESAGLIKKNFGLNGTTKDIESNPKDLKIKAVDAQ 184	XX CC	genome and/or plasmids; and identifying an expression modulating fragment
Qy	163 KSNRGITDVLRLSKQAQFTVFNKGTKKVIDLK 196	XX CC	of the Staphylococcus genome and/or plasmids. The methods and
Db	185 QTARALSDVDISVINNGVATKAGDAKKDPIYLE 218	XX CC	compositions of the present invention are useful for the diagnosis,
		XX CC	prevention and/or treatment of an Staphylococcal epidermidis bacterial
		XX CC	infection. This is the amino acid sequence of a S. epidermis protein of
		XX CC	the invention.
		XX SQ	Sequence 288 AA;
			Query Match 10.7%; Score 108.5; DB 8; Length 288;
			Best Local Similarity 20.6%; Pred. No. 0.4;
			Matches 44; Conservative 43; Mismatches 78; Indels 49; Gaps 6;
RESULT 35			
ADS07354			
ID	ADS07354 standard; protein; 288 AA.	Qy	9 HGSQIPYITVNGTSQNILSLTFNKNQOISYKDIEKNVKSVLVFNRGISDIDLRLSKQ 68
XX		Db	28 NNGKKVTIGVASNDTK-----AWEKVKELAKKD-----DIDLEIKHF 64
XX AC	ADS07354;	Qy	69 AKYTVHFKNGTKRVVDLKAGIHTA-----DLINTSDIKAISVNVDTKKQVK 114
XX XX		Db	65 SDYVNPKNALSDGIDIDLNAFQHFALDQYKKAHDTNIEALSTTVLAPLGIYSKVKNIK 124
DT	04-NOV-2004 (first entry)	Qy	115 DKEAKANYQVPTITVNGTSQNILSN---LTFKKNQOI--SYKOLENNVKSV-----L 162
DE	Staphylococcus epidermis polypeptide seqid 6649.	Db	125 DVKGAQVAIPNDVSNQARALKLLESAGLIKKNFGLNGTTKDIESNPKDLKIKAVDAQ 184
XX		Qy	163 KSNRGITDVLRLSKQAQFTVFNKGTKKVIDLK 196
XX		Db	185 QTARALSDVDISVINNGVATKAGDAKKDPIYLE 218
KW	antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;		
KW	recombinant expression vector; infection; computer readable medium;		
XX	computer based system.		
OS	Staphylococcus epidermidis.		

Db	2	AHHHHHPGGSGGTATVTSVIDNIILSKI--ENEYEVLYLKPLAGVYVRSKKQLEN--N	56
Qy	51	VLYFNRGISDI-DLRLSKQ-----AKYTV-----HFKNGTRKRVVDLK	86
Db	57	VMTFNVNVKDIILNSRFNKRNFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLS	116
Qy	87	AGIHTADLINT-----SDIKALSVNVDTKKQVKDKKEAKANVOVPY	126
Db	117	SYNYIKSDSIDTINFANDVLGYKYVSEKYKSOLDSI-----KKYINDKQGENEKLDPF	170
Qy	127	TITVNGTSQNI-----LSNLTFFKK-NOQISYKDLNNVKS-----LKSN	165
Db	171	LNNIETLYKTVNDKIDL.FVIHLEAEVLNYTYKSNVEVKIKEL-NYLKTIQDKLADFPKN	229
Qy	166	R-----GTTVDVL-----RLSKQAKFTVNFKNGTKKVI	193
Db	230	NNFVGIGADLSTDYNNHNNLLTKFLSTGVMFENPAKTVL	266
RESULT 37			
ID	AAR13992		
XX	AAR13992 standard; protein; 493 AA.		
XX	AAR13992;		
DT	05-DEC-1991 (first entry)		
DE	P. falciparum sporozoite antigen fusion polypeptide.		
XX	Vaccine; NXY gene; malaria; antibodies; purification; affinity.		
KW	Plasmodium falciparum.		
OS	Location/Qualifiers		
PH	Key	1. .21	
FT	Region	/label= A	
FT		/note= "affinity peptide including 6 His residues"	
FT	Region	22. .483	
FT		/label= B	
FT		/note= "amino acids 1-462 of the peptide in AAR13991"	
FT	Region	484. 493	
FT		/label= C	
FT		/note= "vector-encoded peptide"	
XX	EP447956-A.		
XX	25-SEP-1991.		
XX	14-MAR-1991; 91EP-00103920.		
XX	23-MAR-1990; 90CH-00000970.		
XX	(HOFF) HOFFMANN-LA ROCHE AG.		
XX	Certa U, Guttinger M, Matile H;		
XX	WPI; 1991-282989/39.		
XX	New antimalarial polypeptide(s) - corresp. to specific epitope(s) of the		
XX	plasmodium falciparum sporozoite antigen, and are useful as vaccines or		
XX	to prepare antigens.		
XX	Claim 2; Page 18; 36pp; German.		
XX	Vector pDS56/RBSII, 6xHis is a derivative of pDS56/RBS (EP-282042). It		
CC	comprises an additional sequence encoding six histidine residues. Into		
CC	this vector may be ligated a 1400 bp AseI fragment of NXY (see AAQ13727)		
CC	to yield pDS-NXY. E. coli SG13009 (pUHAI) transformed with pDS-NXY		
CC	produces a 69 kD fusion protein comprising the NXY fragment N-terminally		
CC	linked to an affinity peptide contg. 6 His units, and C-terminally to a		
CC	vector-derived sequence. Fragment B corresponds to amino acids 1-462 of		
CC	the N-terminal of the sporozoite antigen. The affinity peptide is used		
CC	for the purification of the antigen. The polypeptide is useful for the		

RESULT 36	
ADE24164	
ID	ADE24164 standard; protein; 371 AA.
XX	
AC	ADE24164;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Plasmodium falciparum (FVO) MSP-1 42 protein SEQ ID NO:5.
XX	
KW	merozoite surface protein; MSP-1 42; Plasmodium falciparum;
KW	Plasmodium falciparum FVO; antimalarial, vaccine; malaria;
KW	malaria infection.
XX	
OS	Plasmodium falciparum.
XX	
PN	WO2003084472-A2.
XX	
PD	16-OCT-2003.
XX	
PF	01-APR-2003; 2003WO-US010385.
XX	
PR	01-APR-2002; 2002US-0369741P.
PR	09-MAY-2002; 2002US-0379688P.
XX	
PA	(REED-) REED ARMY INST RES WALTER.
XX	
PI	Angov E, Lyon JA, Darko CA, Cohen JD;
XX	
DR	WPI; 2003-876999/81.
XX	
PT	New recombinant MSP-142 protein that retains its native folding, useful
PT	for preparing a vaccine against malaria infection.
XX	
PS	Disclosure; SEQ ID NO 5; 91pp; English.
XX	
CC	The present invention describes a recombinant merozoite surface protein
CC	(MSP)-1 42 protein, that retains its native folding. Also described: (1)
CC	a composition comprising the recombinant Plasmodium falciparum FVO MSP-1
CC	42; (2) a recombinant vector comprising a DNA sequence encoding the
CC	recombinant Plasmodium falciparum FVO MSP-1 42; (3) a host cell
CC	transformed with the vector; (4) producing and purifying recombinant
CC	Plasmodium falciparum FVO MSP-1 42 proteins in a culture medium; (5)
CC	producing and purifying recombinant Plasmodium falciparum FVO MSP-1 42
CC	protein; (6) an antibody produced against the recombinant Plasmodium
CC	falciparum FVO MSP-1 42 protein; (7) in vitro diagnosis or detection of
CC	malaria antigen present in a biological sample; (8) a kit for in vitro
CC	detection of a malaria antigen present in a biological sample; (9) an
CC	immunogenic carrier comprising the recombinant Plasmodium falciparum FVO
CC	MSP-1 42 protein; (10) in vitro diagnosis of malaria antibodies in a
CC	biological sample; (11) a kit for determining the presence of malaria
CC	antibodies in a biological sample; (12) in vitro monitoring of malaria
CC	infection or prognosing the response to treatment of patients suffering
CC	from malaria infection; (13) a kit for monitoring malaria infection or
CC	prognosing the response to treatment of patients suffering from malaria
CC	infection; (14) a vaccine against malaria comprising Plasmodium
CC	falciparum FVO MSP-1 42; and (14) inducing an immune response against
CC	malaria infection. MSP-1 42 has antimalarial activity, and can be used in
CC	vaccines. The recombinant MSP-1 42 protein is useful for preparing a
CC	vaccine against malaria infection. The present sequence represents
CC	Plasmodium falciparum (FVO) MSP-1 42, which is used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 371 AA;
Query Match	10.7%; Score 108.5; DB 7; Length 371;
Best Local Similarity	21.7%; Pred. No. 0.56;
Matches	60; Conservative 39; Mismatches 79; Indels 99; Gaps 150
YQ	4 SHHHHHH-GSQIPPTITVNGT*SQNILSLTFNKNQIQSY-----KDIENKVKYS 50
	: : : : : : : : : : :

```
CC prodn. of antimalarial vaccines. See also AAQ13727-8
XX Sequence 493 AA;
SQ
  Query Match      10.6%; Score 107.5; DB 2; Length 493;
  Best Local Similarity 25.4%; Pred. No. 1;
  Matches 50; Conservative 24; Mismatches 72; Indels 51; Gaps 9;
QY 1 MRGSHHHHHSQIPYTTVNGTSQ--NILSSLTFNKNQOISYKDIENKVKSVLYFNRI 58
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MRGSHHHHHSQIPYTTVNGTSQ--NILSSLTFNKNQOISYKDIENKVKSVLYFNRI 58
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 59 SDIDLRLSKQAKY---TVHFKNGTGRVVLDLKGAIHTADLINTSDIKASVNVDTKKQVKD 115
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 53 NKTNVLSKLNNAVYKNSVHKMNAVNVK-----NAVKNVNAV-----KVNVNKKDILN 101
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 KEAKANVQVPYTTVNGTSQNILSLTFNKNQOISYKDIENKVKSVLKSNRGITDVLRL 175
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 102 K-----LNALYKNNAVYKKNAL--NKVSAVNK-----VSAVNKVS 134
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 SKQAKFTVNFKNGTKKV 192
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 AVNKMGAVRNVGNVKV 151
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 38
AAW31555
ID AAW31555 standard; protein; 345 AA.
XX
AC AAW31555;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
XX Fibronectin-binding MSCRAMM derivative pCF33.
XX
KW Fibronectin; pCF33; collagen binding protein; sepsis; infection;
KW microbial surface component recognising adhesive matrix molecule; MSCRAMM;
KW adhesin; vaccine; immunisation; diagnosis; therapy; mastitis.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Peptide 1..12
  /note= "vector pQE30-derived peptide"
XX
XX WO9743314-A2.
XX
XX 20-NOV-1997.
XX
XX 14-MAY-1997; 97WO-US008210.
XX
XX 16-MAY-1996; 96US-0017678P.
XX
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX (UABR-) UAB RES FOUND.
XX
XX Hosceek M, Patti JM, House-Pompeo K, Sthanam N, Symersky J;
XX WPI, 1998-008801/01.
XX
XX Antibody that interacts with collagen binding domain of Staphylococcal
XX cna gene product - useful to prevent bacterial sepsis in animal infected
XX with Staphylococcus aureus.
XX
XX Disclosure; Page 91; 143pp; English.
XX
XX This protein comprises Staphylococcus aureus fibronectin-binding
XX microbial surface component recognising adhesive matrix molecule (MSCRAMM)
XX derivative pCF33, plus a vector-derived N-terminal peptide. The invention
XX relates to claimed nucleic acid sequences (see AAT93436-38) encoding S.
XX aureus collagen binding protein (CBP) epitopes M17, M31 and M55 (see
```

```
CC AAW31552-54) that confer protection against S. aureus infection. CBP
CC protein and antigenic epitopes are contemplated for use in the treatment
CC of pathological infections, especially to prevent bacterial adhesion to
CC collagen. The epitopes are also contemplated for use in the preparation
CC of vaccines and as carrier proteins in vaccine formulations, as well as
CC in the formulation of compositions for the prevention of S. aureus
CC infection. pCF33 and pQD (see AAW31556) were used to raise anti-MSCRAMM
CC polyclonal antibodies used in passive immunisation against bovine
CC mastitis. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX AUG-2003 to correct OS field.)
XX
SQ Sequence 345 AA;
  Query Match      10.4%; Score 106; DB 2; Length 345;
  Best Local Similarity 23.3%; Pred. No. 0.83;
  Matches 52; Conservative 35; Mismatches 90; Indels 46; Gaps 11;
QY 1 MRGSHHHHHSQIPYTTVNGTS--QNTLSSLTFNKNQOIS--YKDIENKVKSVLYP--N 55
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MRGSHHHHHSQIPYTTVNGTS--QNTLSSLTFNKNQOIS--YKDIENKVKSVLYP--N 55
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 56 RGISDIDLRLSKQAKYTVHFKNGTGRVVLDLKGAG-----IHT-ADLINT-S 98
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 SAVKGDTEKIVPKELNLNGVTSTAKVPPIMAGDQVLANGVIDSGNVITYTDTVNTKD 120
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 99 DIKAI-----SVNVDTKQVKDKAKANYQVP-----YTITVNGTSQNI 137
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 DVKATLTMPAVIDPENVKKTGNVTLATGISTTANKTVLVDYKGYKGFNLSIKGTIDQI 180
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 138 -LSNLTFFKNQOISYKDIENKVKSVLKS-N-RGITDVLRLSKQ 178
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 DKTNTYRTQTYVNPSPG-DNVIAPVLTCNLRPTDSDNALIDQQ 222
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 39
ABM79015
ID ABM79015 standard; protein; 560 AA.
XX
AC ABM79015;
XX
DT 15-JAN-2004 (first entry)
XX
XX Staphylococcus epidermidis SdrG NIN2N3 domain.
XX
XX SdrG; surface protein; infection; antibacterial; vaccine.
XX
XX Staphylococcus epidermidis.
XX
XX WO2003076470-A1.
XX
XX 18-SEP-2003.
XX
XX 05-MAR-2003; 2003WO-US006415.
XX
XX 05-MAR-2002; 2002US-0361324P.
XX
XX (INHI-) INHIBITEX INC.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
XX Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;
XX Robbins J, Vernachio J, Bowden MG;
XX WPI, 2003-722324/68.
XX N-PSDB; ACF06024.
XX
XX New antibody recognizing a Staphylococcus epidermidis protein comprising
XX SdrG NIN2N3, SdrG N2N3 or SdrGR2 useful for preparing a composition for
XX treating or preventing a coagulase-negative Staphylococcal infection.
XX
XX Claim 27; Page 24-25; 78pp; English.
XX
XX The present sequence comprises the protein sequence of the NIN2N3 region
XX (amino acids 50-597), or putative A domain, of the SdrG surface protein
CC
```

